

FIGURE 1

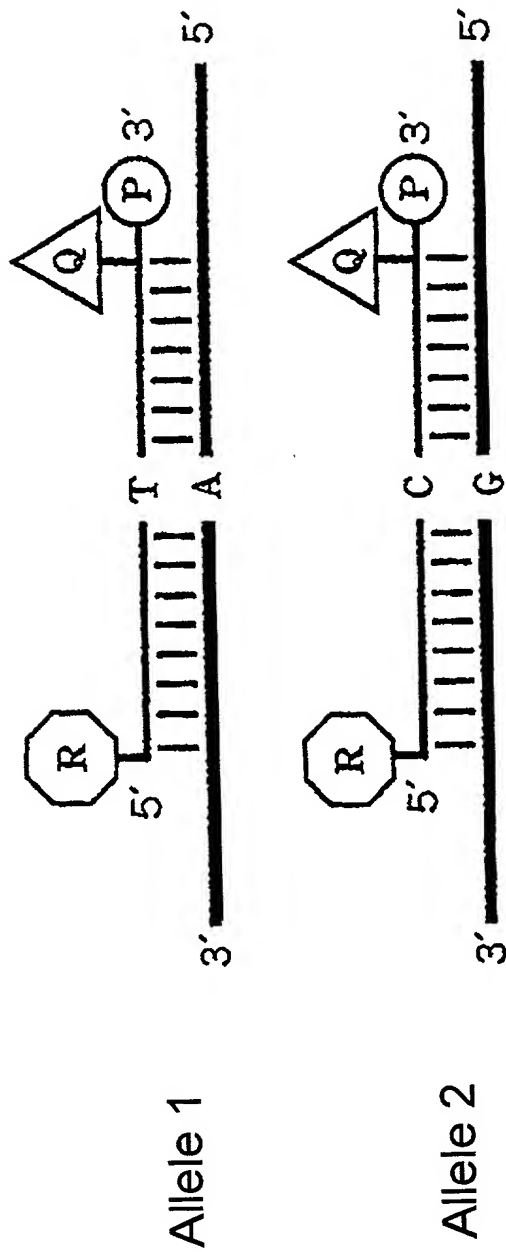


Fig. 302

L1 cell adhesion molecule (L1CAM)

Accession No. U52112

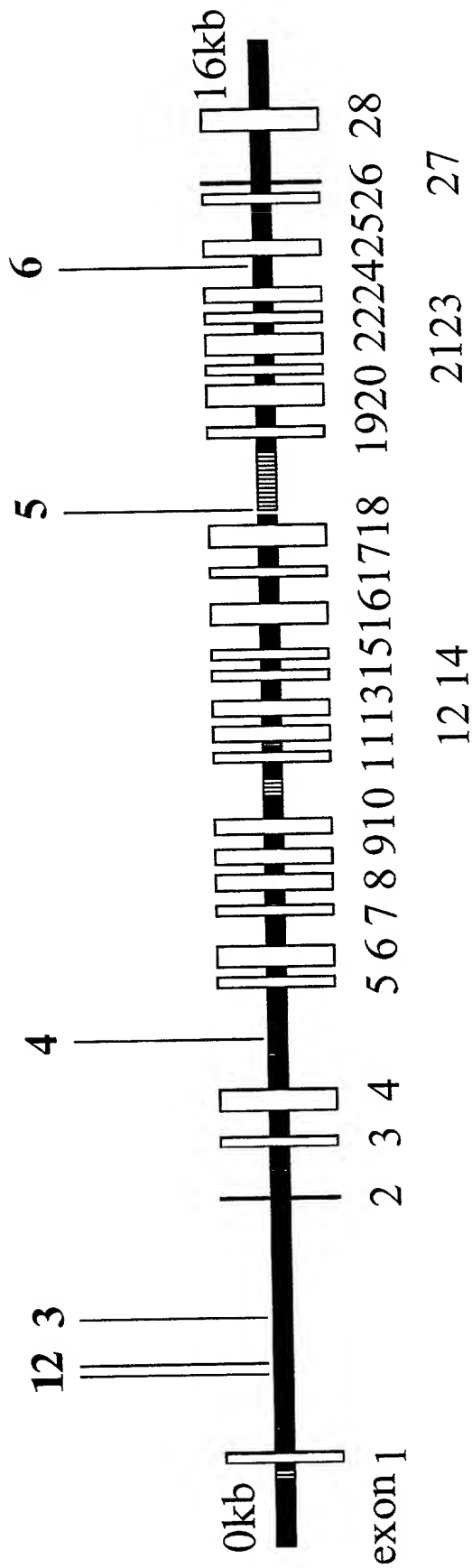


FIGURE 3

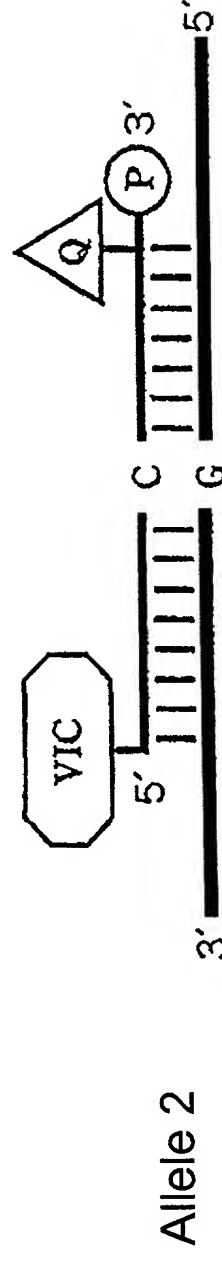
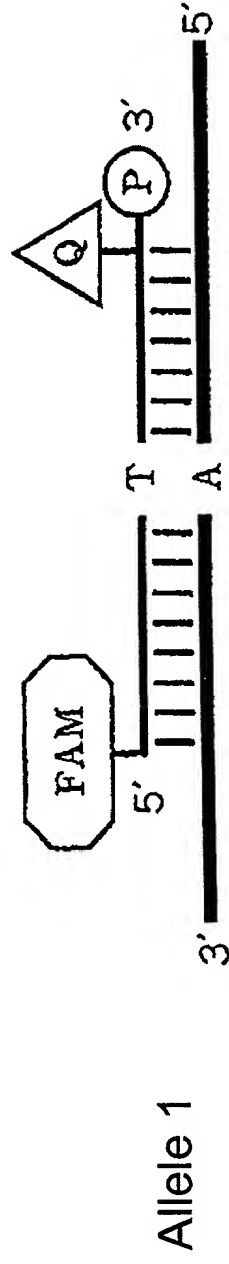


FIGURE 4

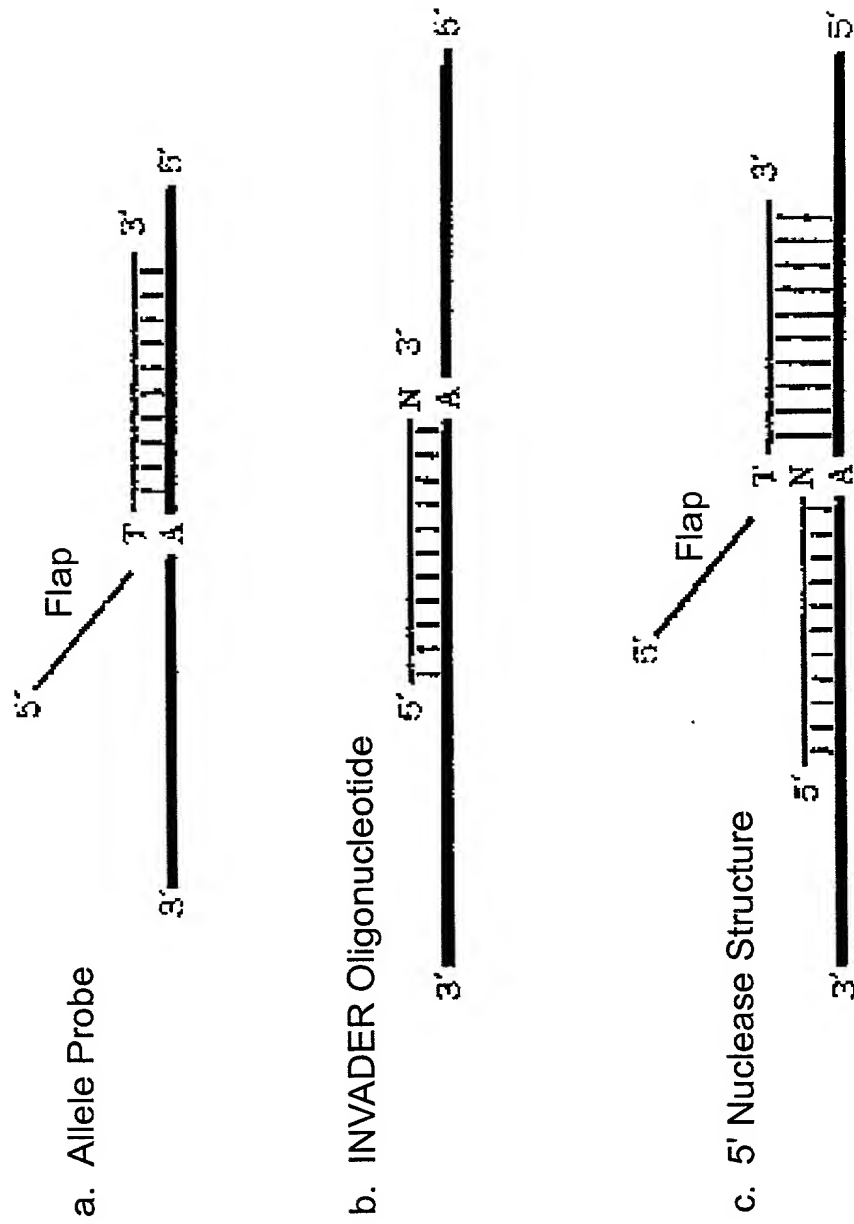


FIGURE 5

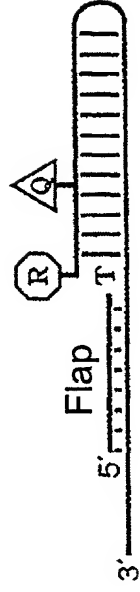
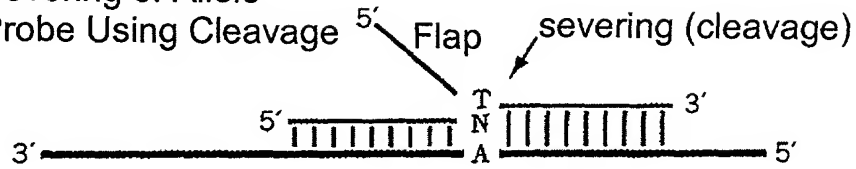
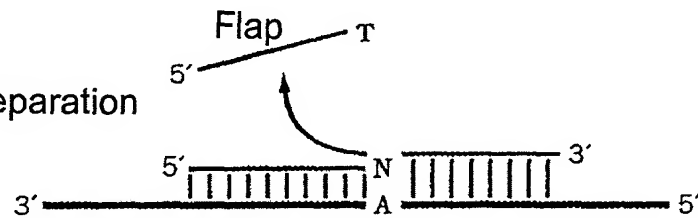


FIGURE 6

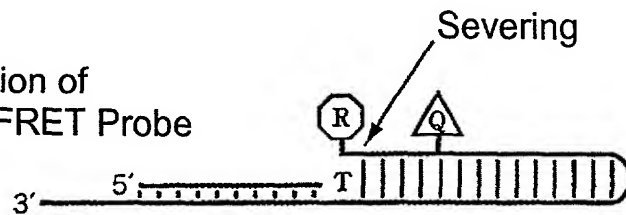
- a. Severing of Allele
Probe Using Cleavage



- b. Flap Separation



- c. Hybridization of
Flap and FRET Probe



- d. Separation of
Fluorescent Dye

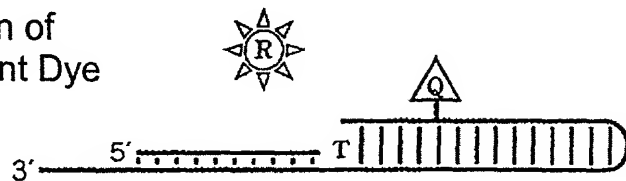


FIGURE 7

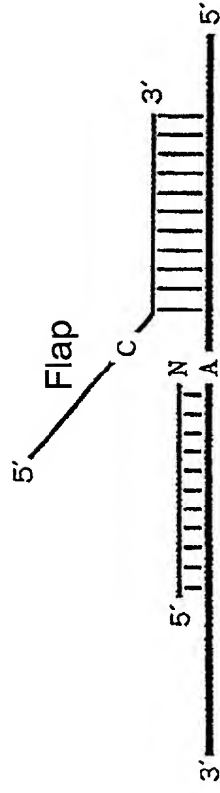
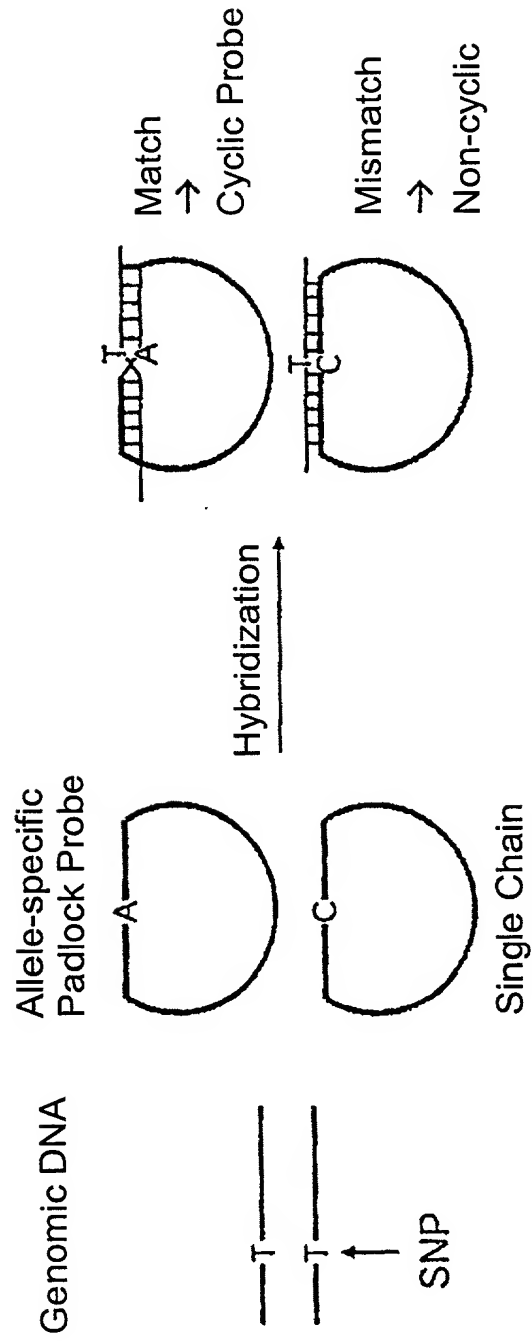


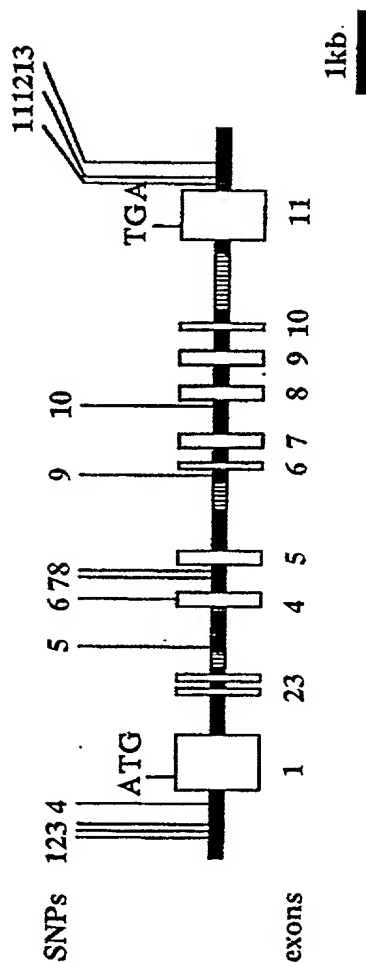
FIGURE 8



ATP binding cassette, sub-family B, member 2 (ABCB2)

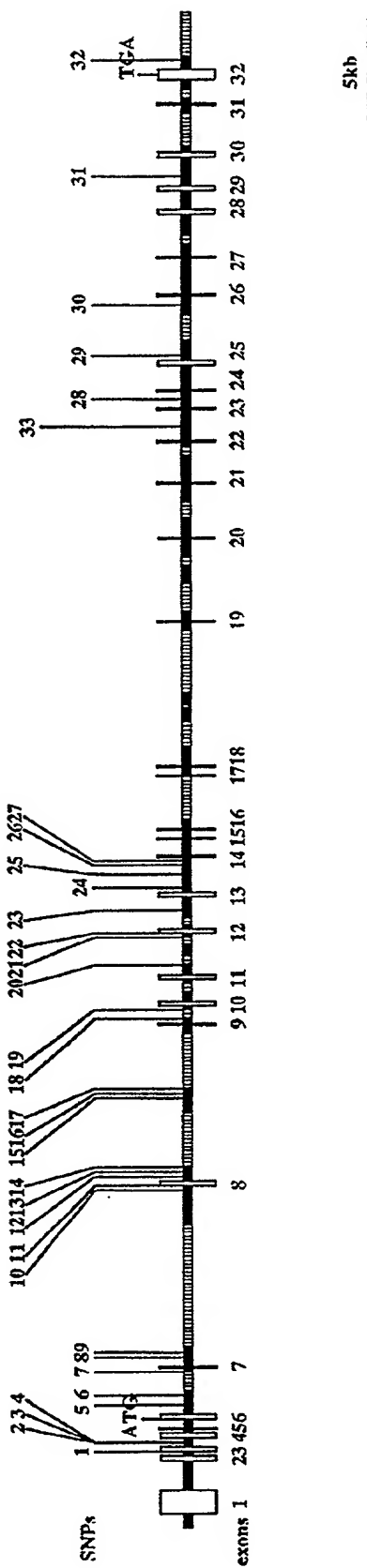
ACCESSION X66401

FIGURE 9



ATP-binding cassette, sub-family B, member 4 (ABCB4)

ACCESSION AC079591
AC079303
AC005045



Epoxide hydrolase 1, microsomal (EPHX1)

ACCESSION AC058782

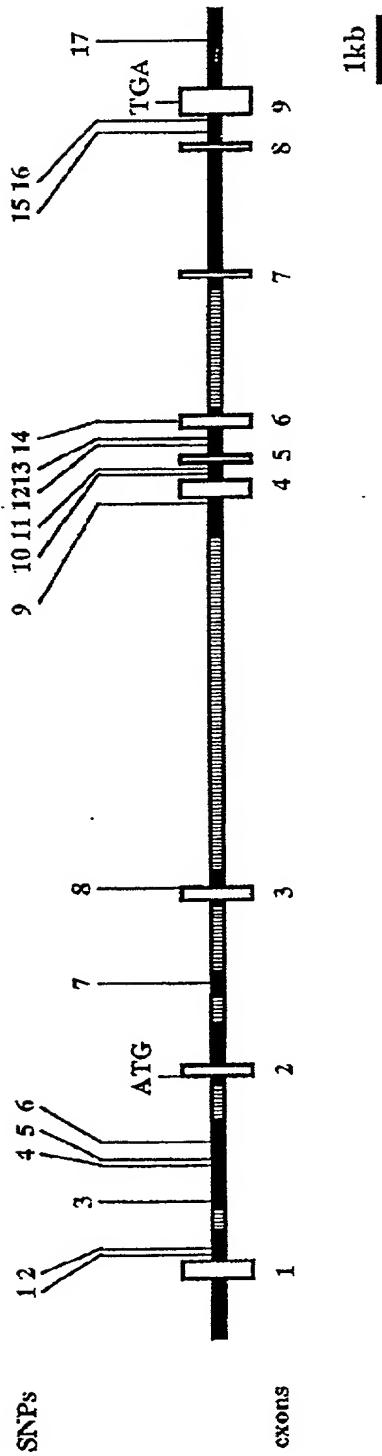
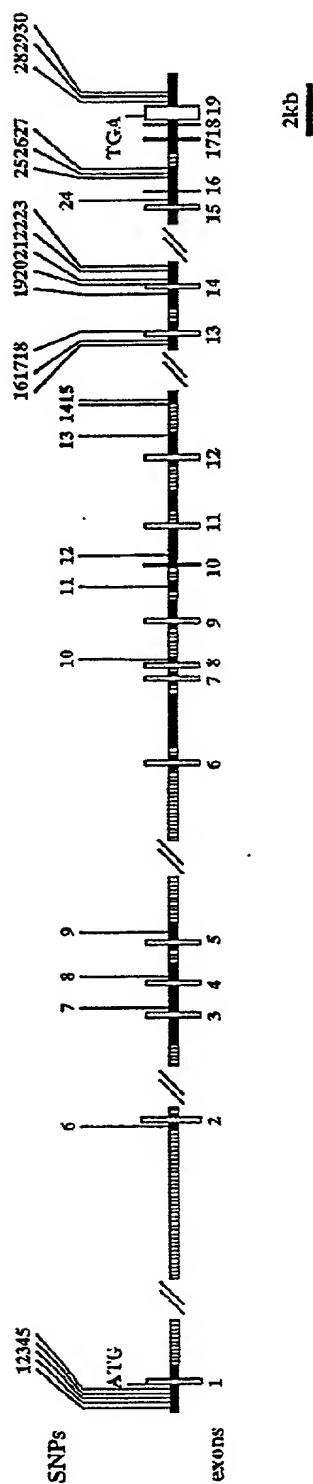


FIGURE 11

FIGURE 12



Epoxide hydrolase, cytoplasmic (EPHX2)

ACCESSION AC010856

Guanidinoacetate N-methyltransferase (GAMT)

ACCESSION NT_000879

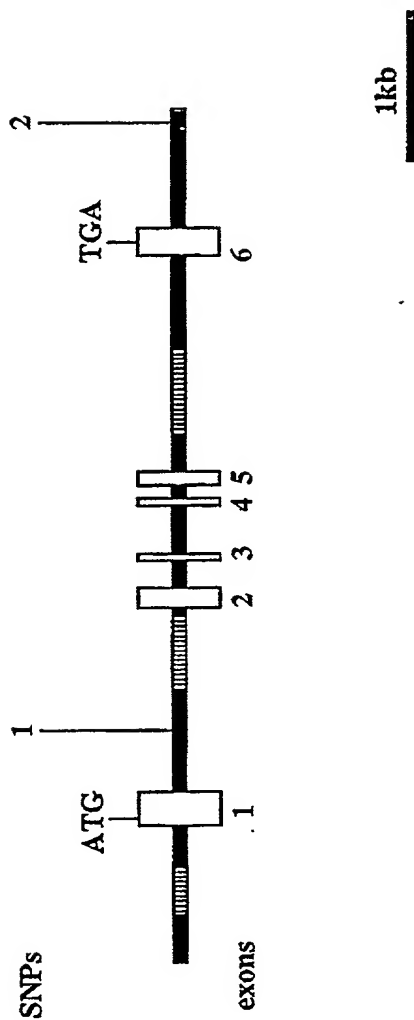


FIGURE 13

Fig. 276

Gamma-glutamyltransferase 1 (GGT1)

ACCESSION D87002.1

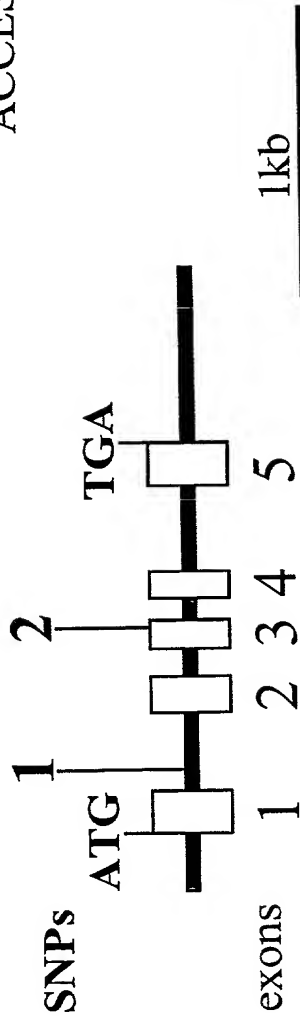
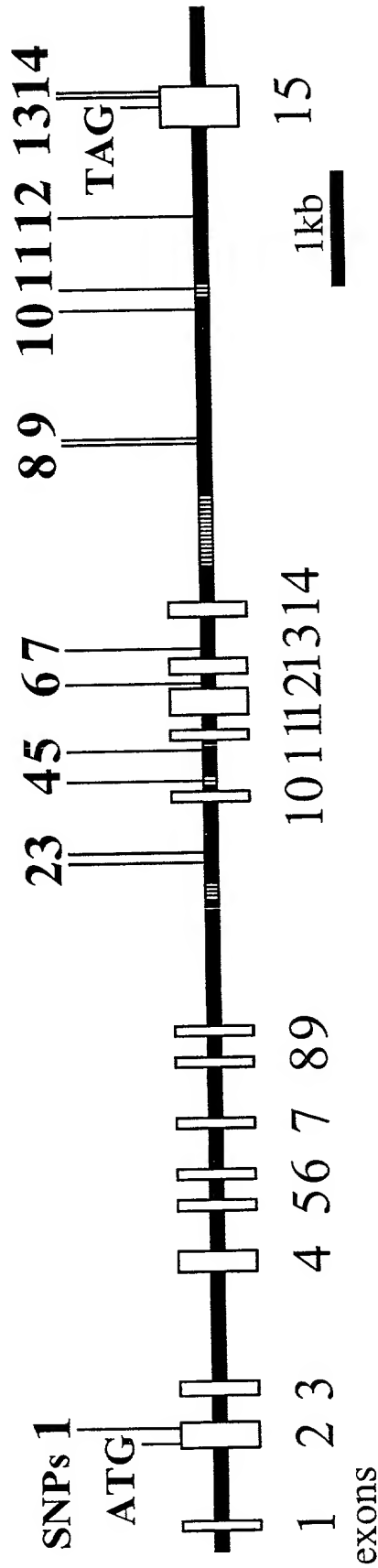


Fig. 277

Transglutaminase 1 (TGMI)

ACCESSION M98447.1



Phenylethanolamine N-methyltransferase (PNMT)

ACCESSION AC040933

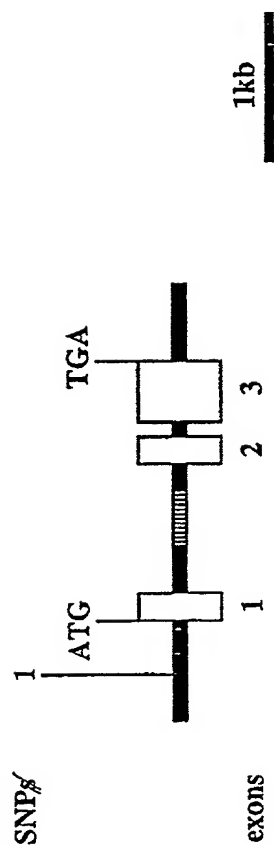


FIGURE 15

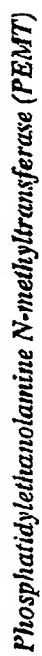


FIGURE 18

Aldehyde dehydrogenase 5 (ALDH5)

ACCESSION AL135785

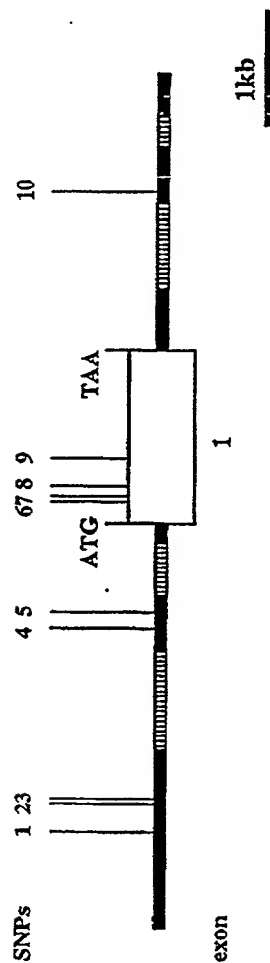
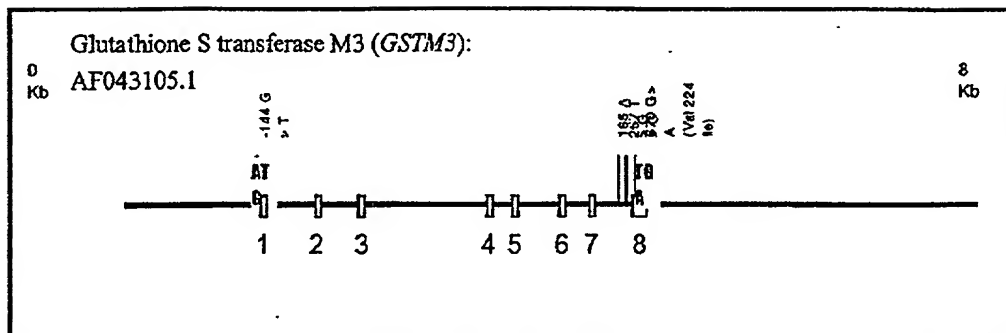


FIGURE 17



Transglutaminase 1 (TGM1)

ACCESSION M98447

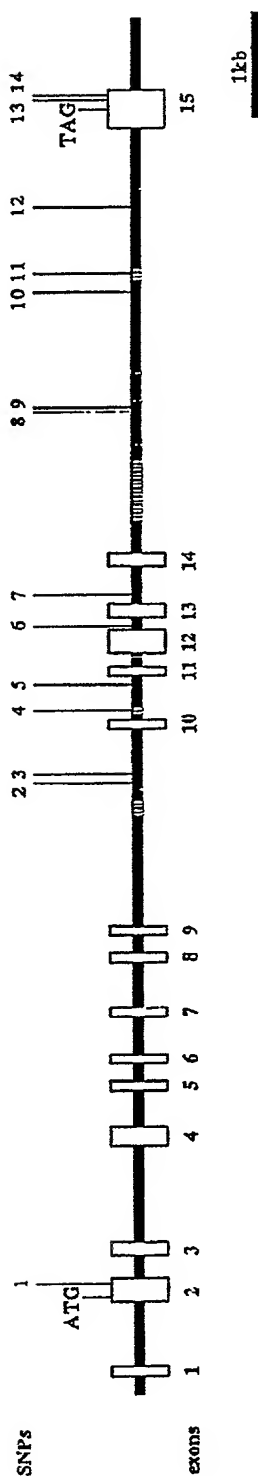


FIGURE 19

Gamma-glutamyltransferase 1 (GGT1)

ACCESSION D87002

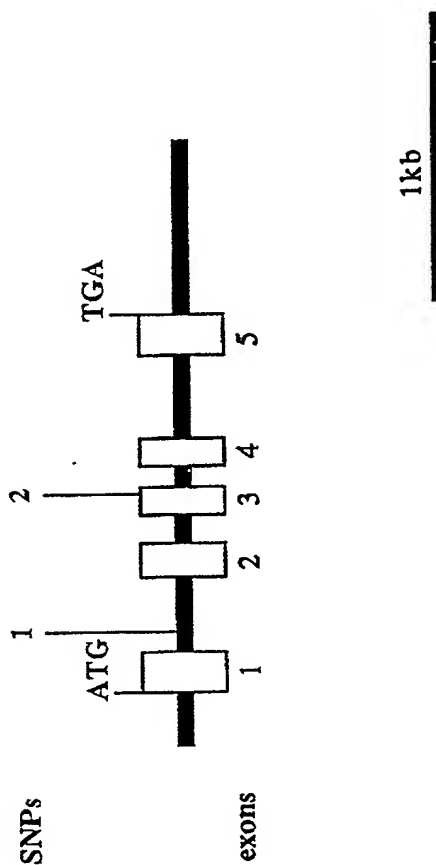


FIGURE 21

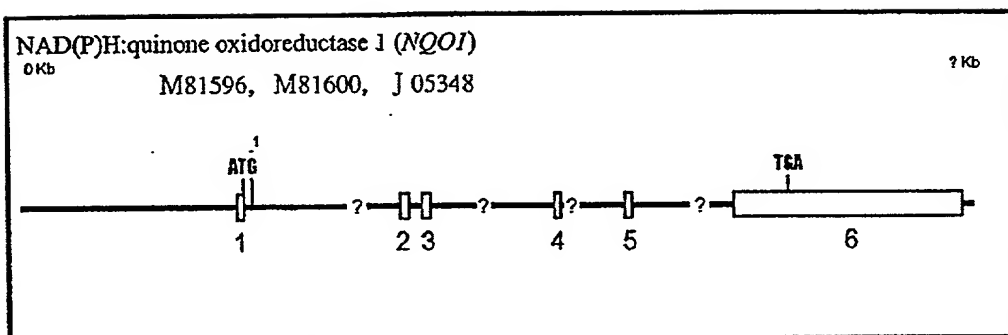


FIGURE 22

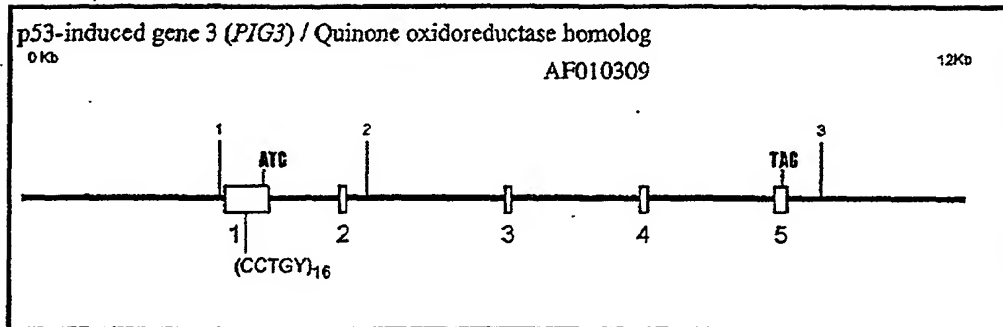


FIGURE 23

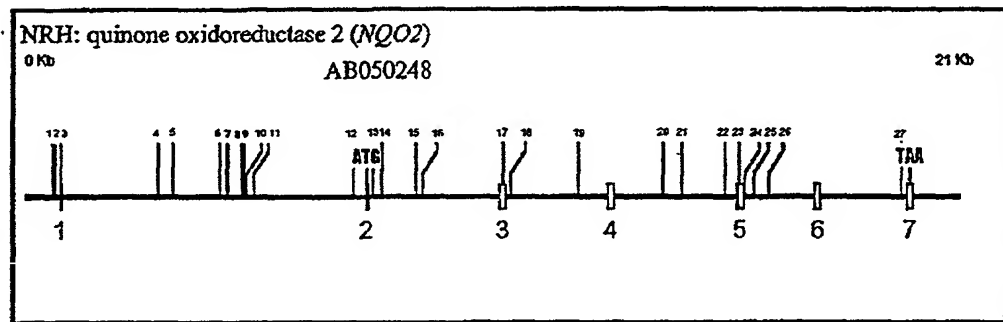


FIGURE 24

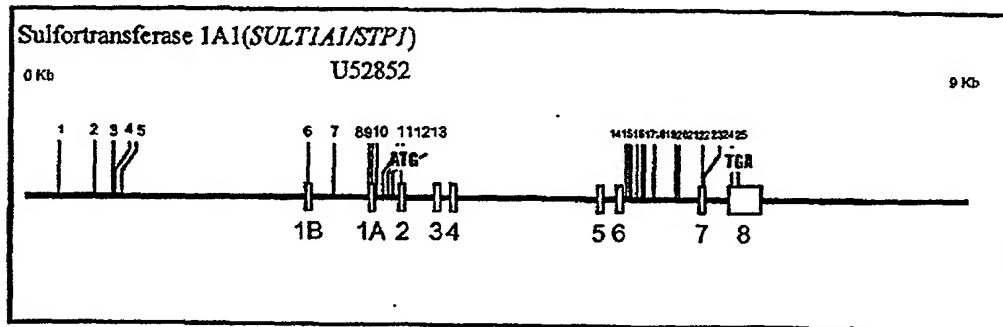


FIGURE 25

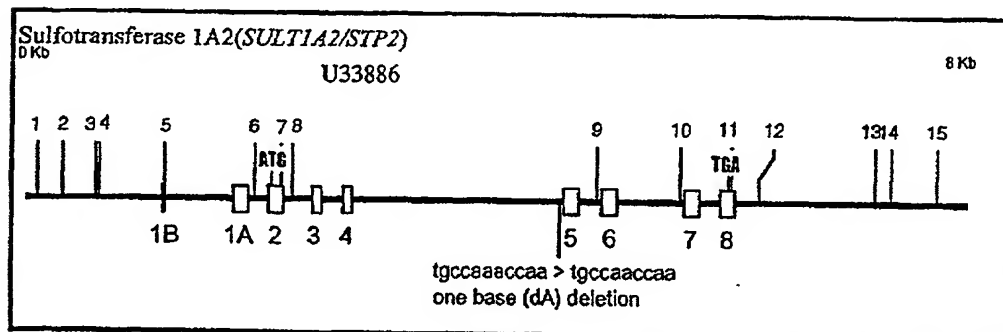


FIGURE 26

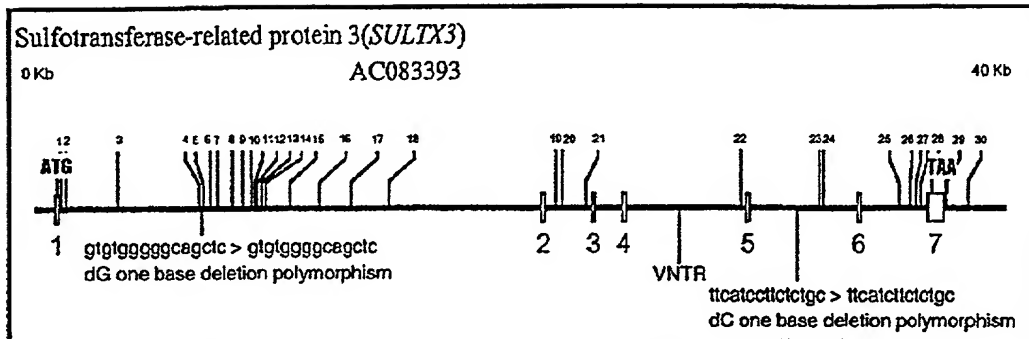


FIGURE 27

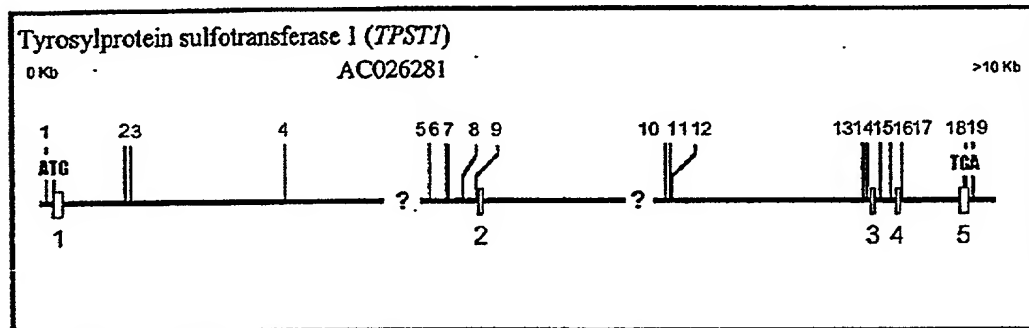


FIGURE 28

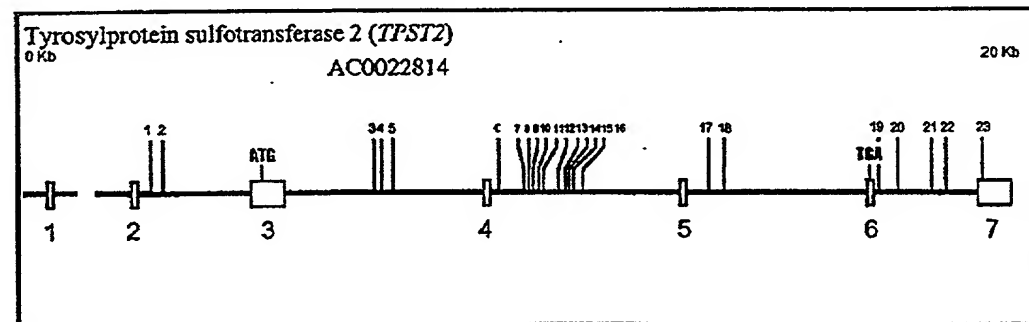
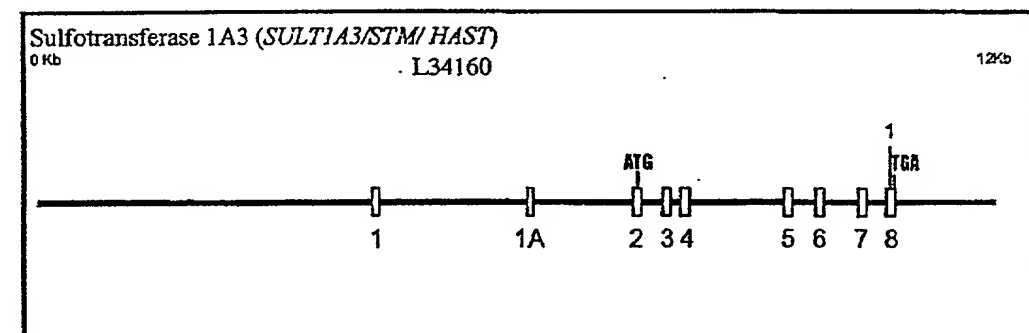
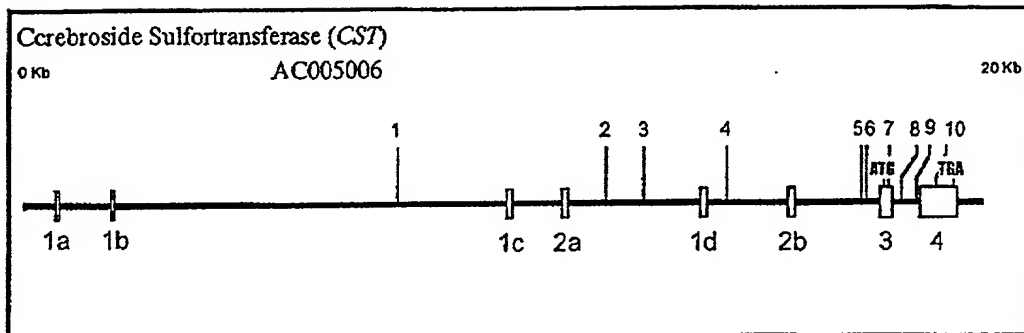


FIGURE 29



	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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【図 3 1】

FIGURE 31

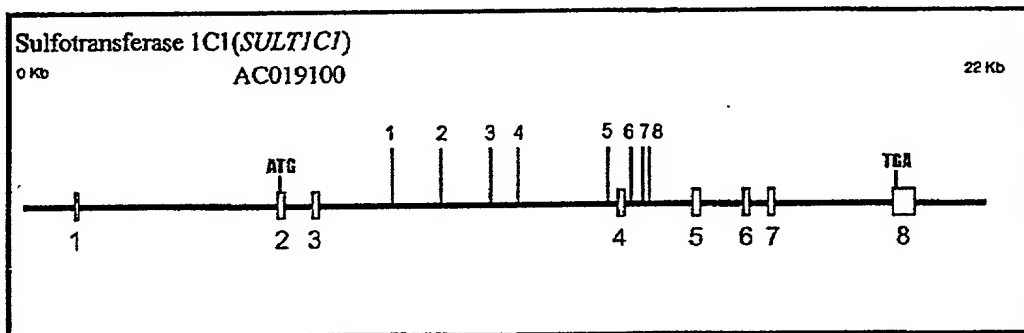


FIGURE 32

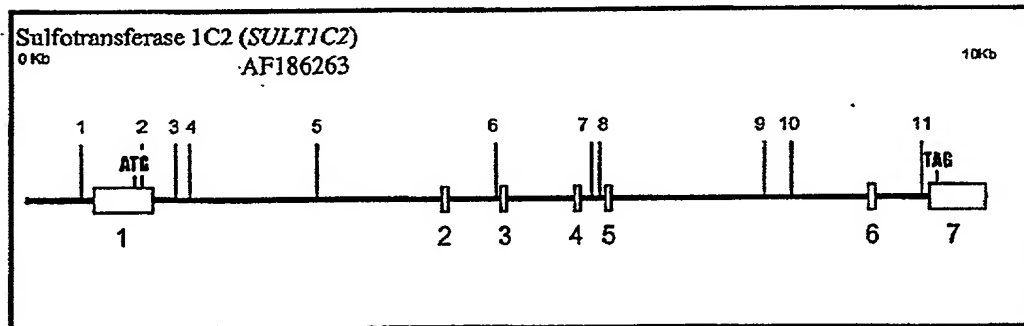
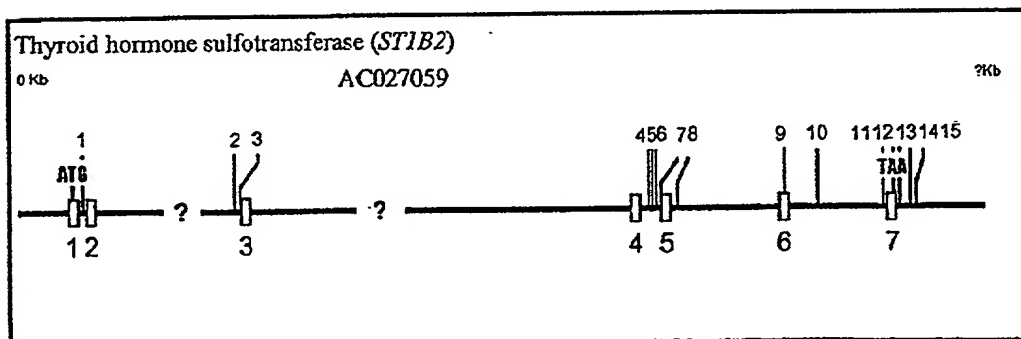


FIGURE 33



Sequence

Observed : G/C
 3' Assay : TCACTCGCTC TTACAGTACC TACCTGCCTA CCTGCCTCTG AGGAGAAACG CTGTAATTAG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_004648.3 (Graphical View of this Entry)
 Chromosome : 1
 map
 Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.
 Position in Sequence : 422012 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_004648.3 20010416_3
 Amplified region : 421033..422147 in NT_004648
 size : 1115

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CGAAGAATAT ACTGCTACGG	T

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105136

12/17/2001

FIGURE 37

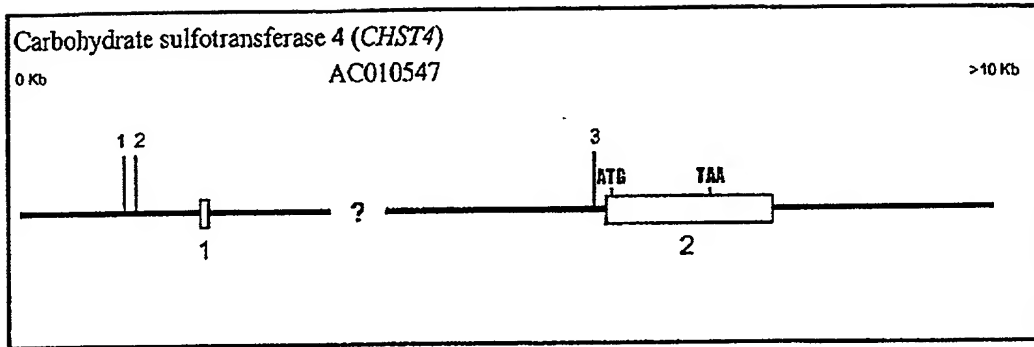


FIGURE 38

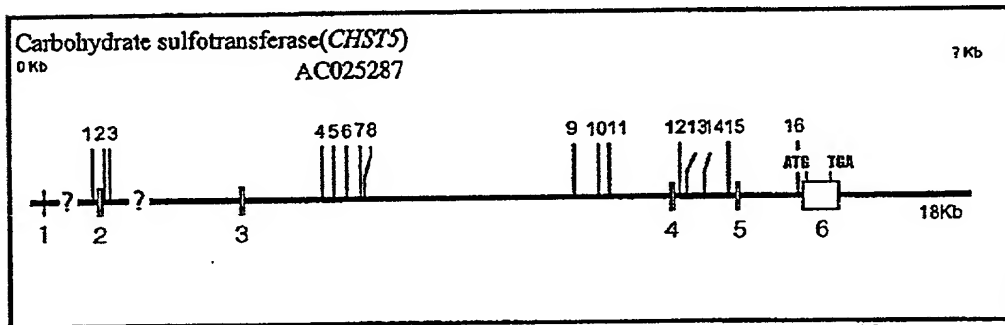


FIGURE 39

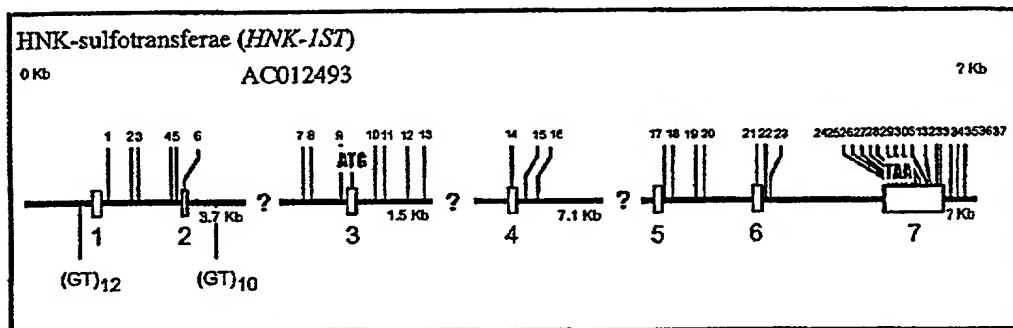


FIGURE 40

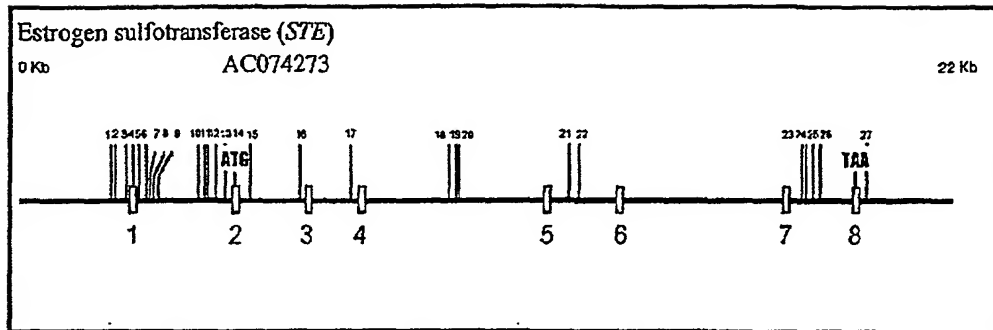


FIGURE 41

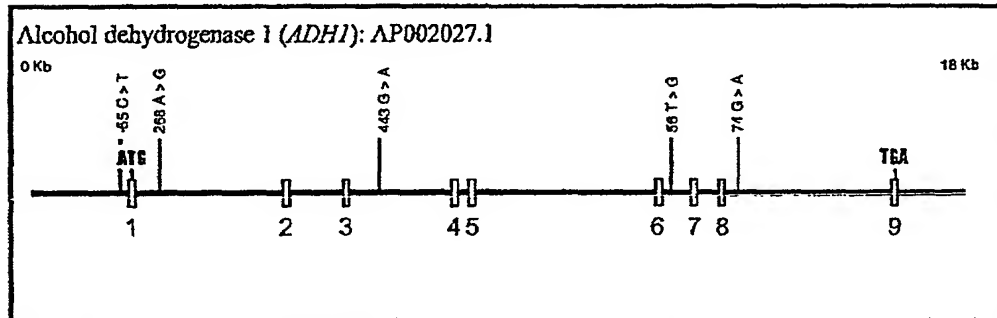


FIGURE 42

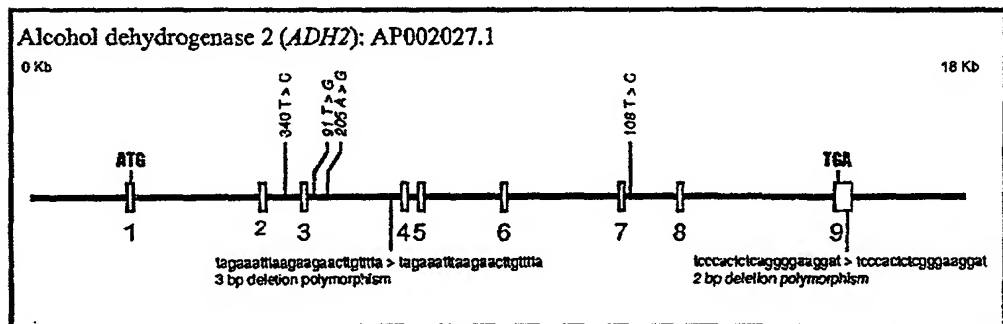


FIGURE 43

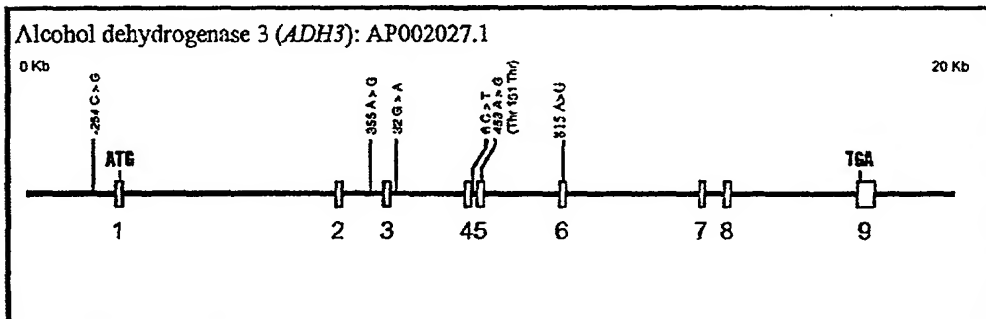


FIGURE 44

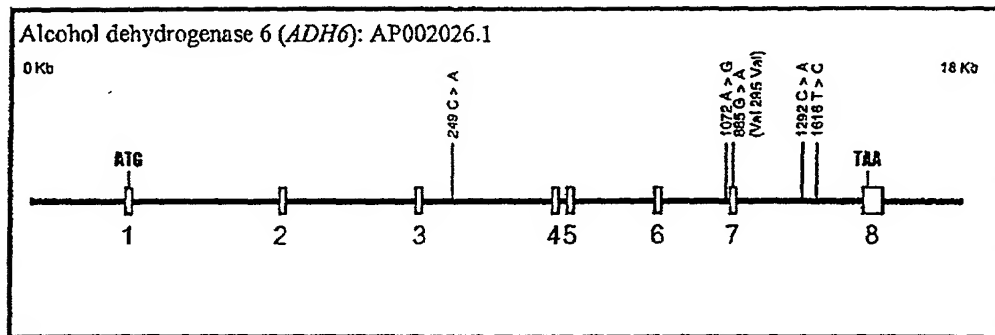


FIGURE 45

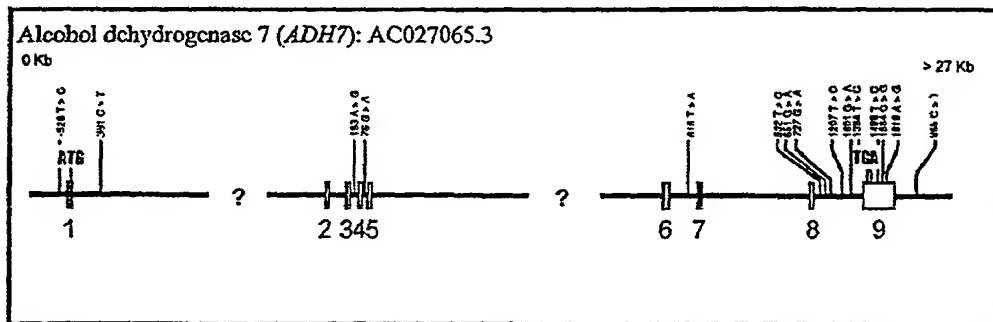
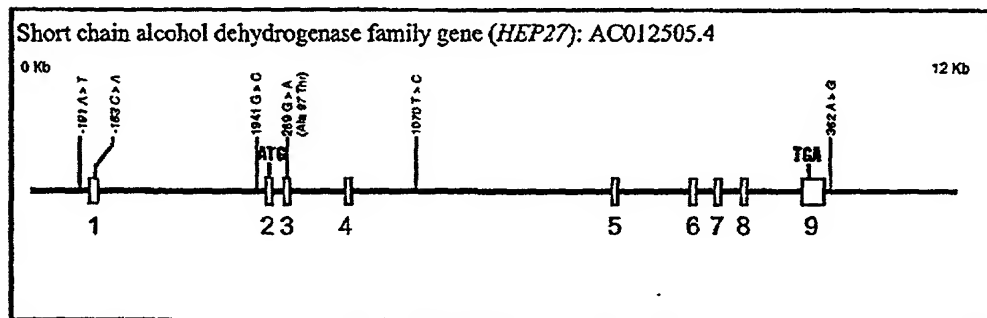


FIGURE 46



arylalkylamine N-acetyltransferase(AANAT)

Accession No. U40391

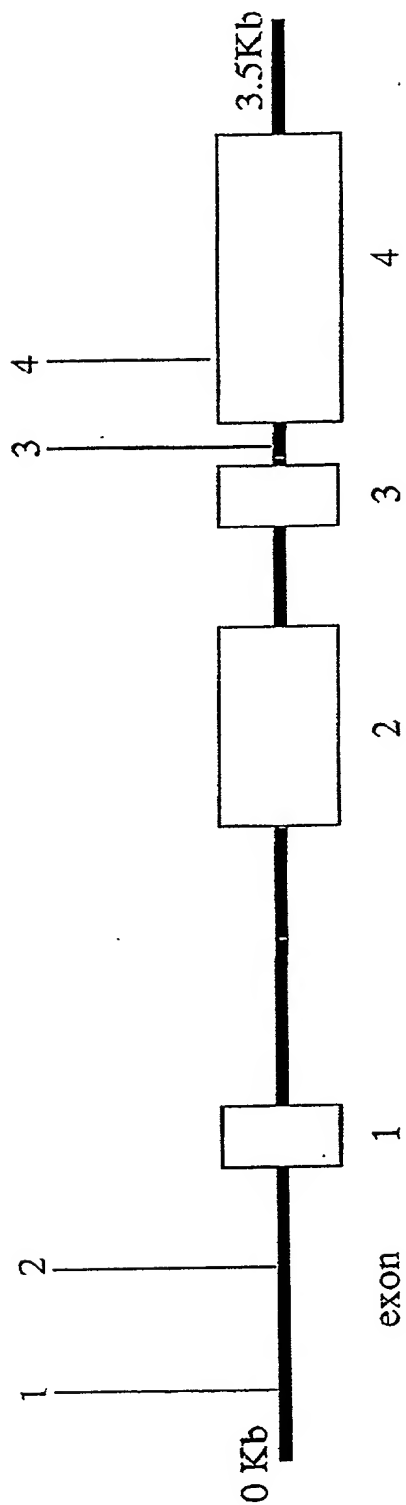


FIGURE 48

N-acetyltransferase, homolog of *S. cerevisiae* (ARD1)

Accession No. U52112

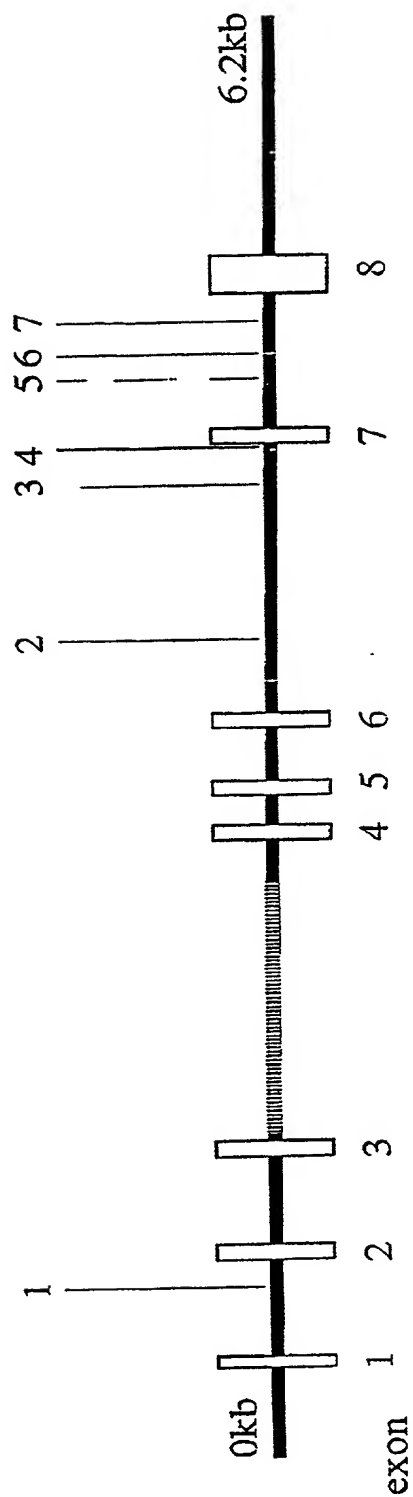


FIGURE 49

N-acetyltransferase (NAT1)

Accession No. X17059

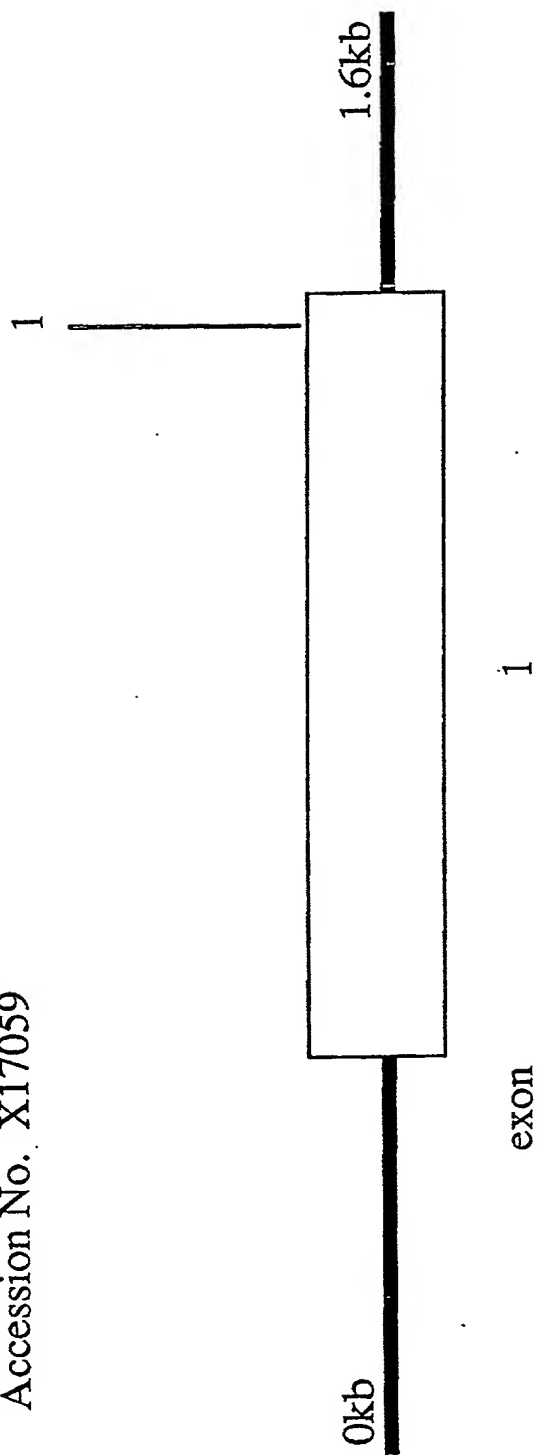


FIGURE 50

arylamine N-acetyltransferase (NAT2) Accession No.: I22255, AC025062, AC025648, D10870

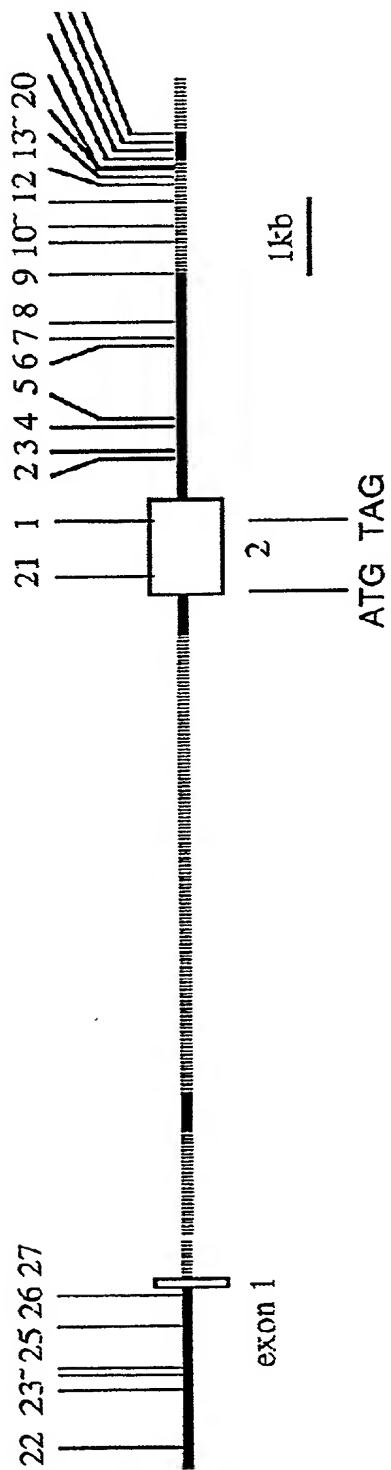


FIGURE 51

Granzyme A (GZMA)

Accession No. AC025790

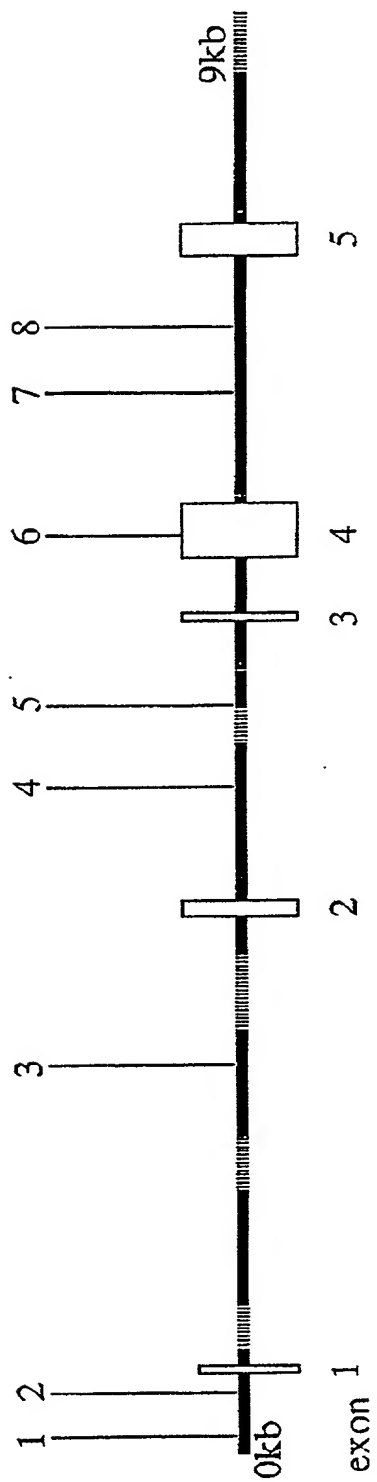


FIGURE 52

Granzyme B (GZMB)

Accession No. M72150

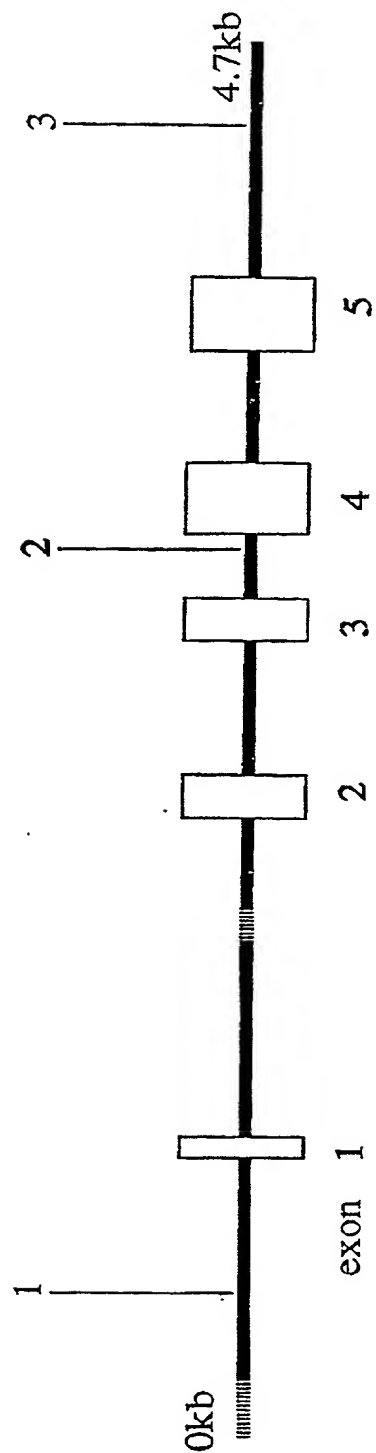
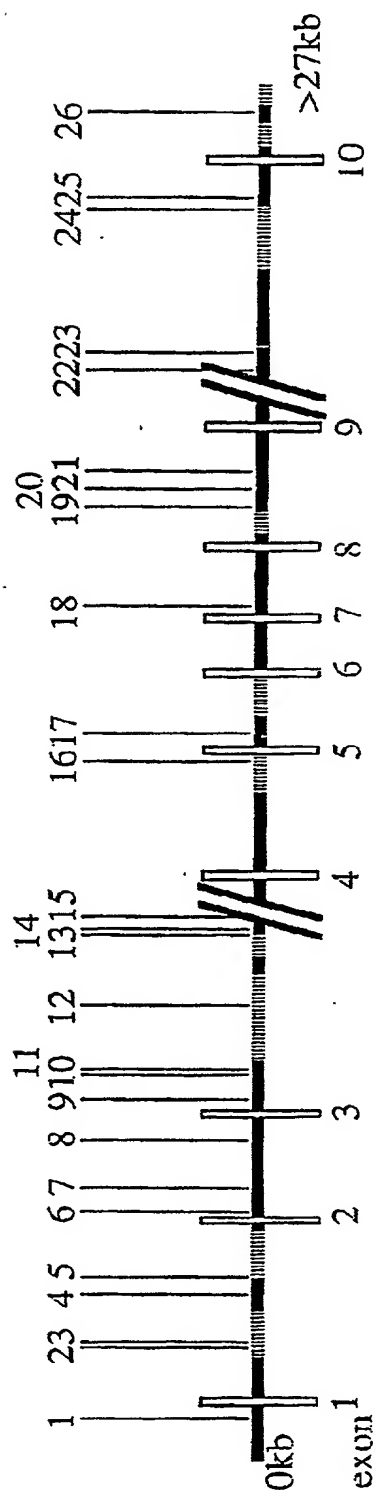


FIGURE 53

esterase D/formylglutathione hydrolase (ESD)

Accession No. AC136958

FIGURE 54



dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST)

Accession No. D89060

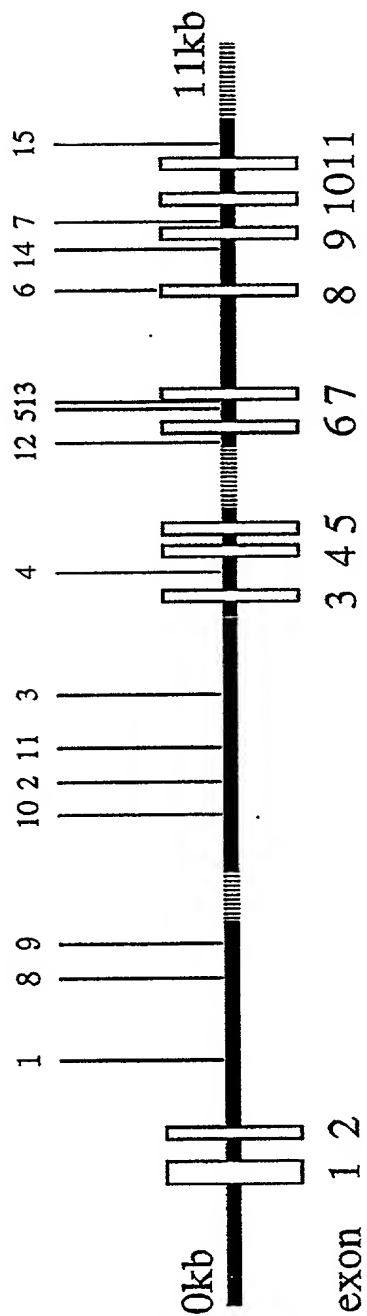


FIGURE 55

FIGURE 60

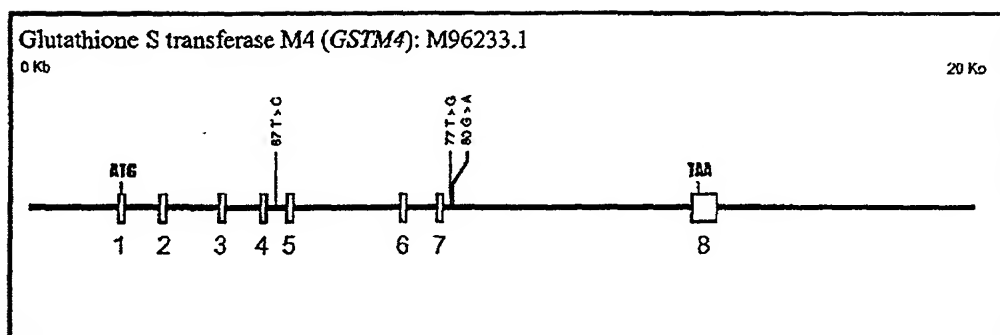


FIGURE 61

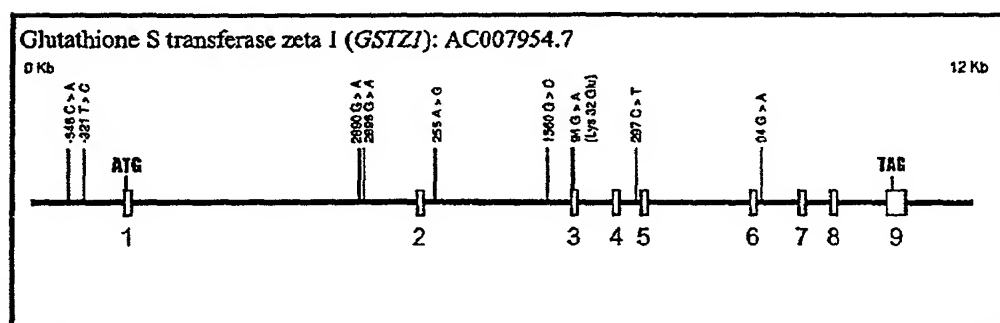


FIGURE 62

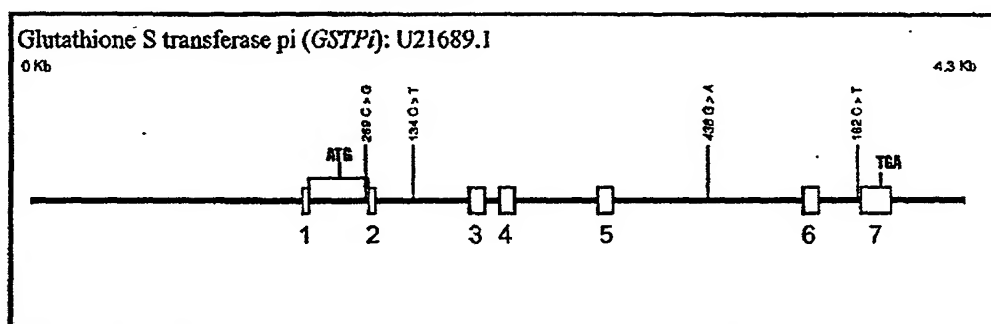


FIGURE 63

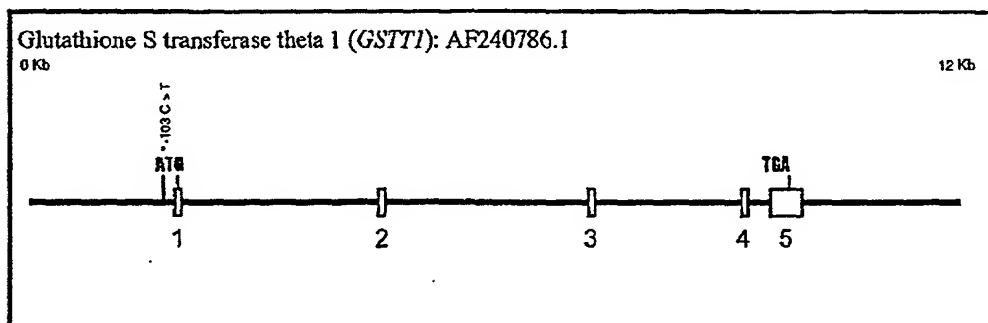


FIGURE 64

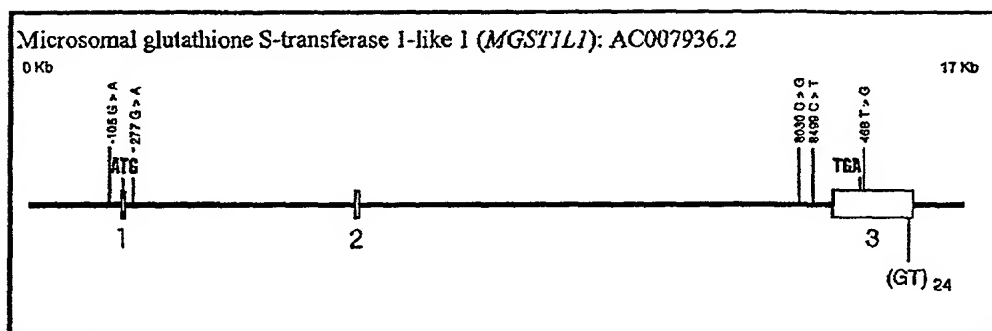


FIGURE 65

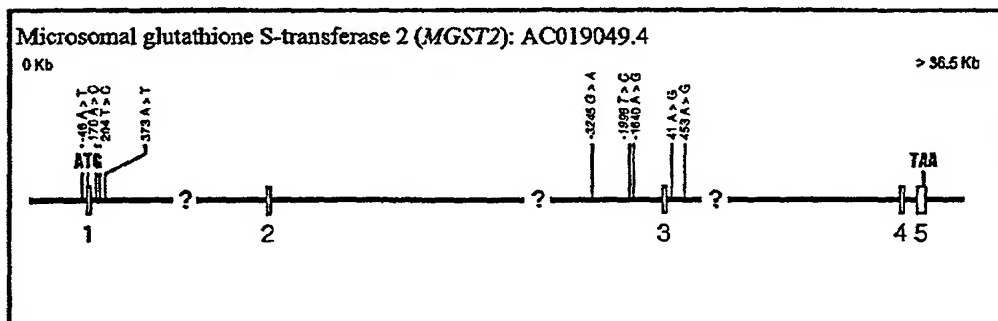


FIGURE 66

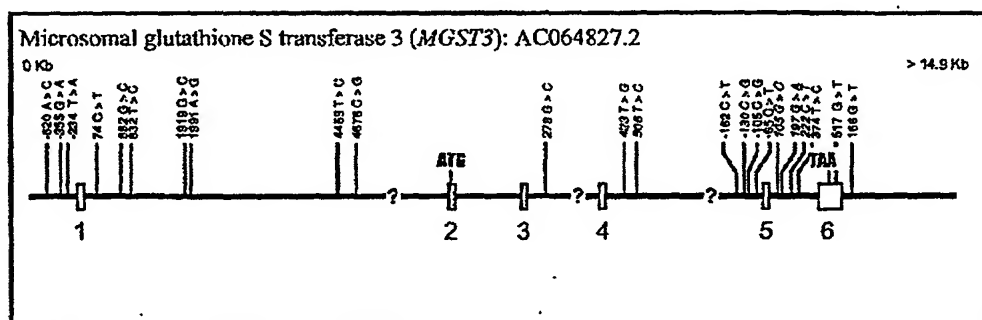


FIGURE 67

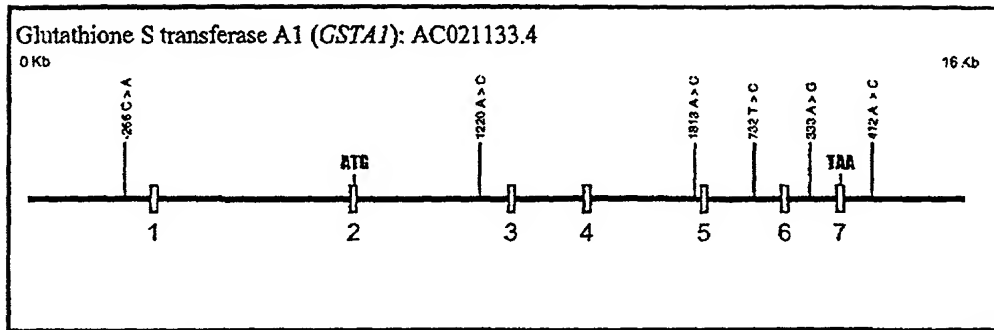


FIGURE 68

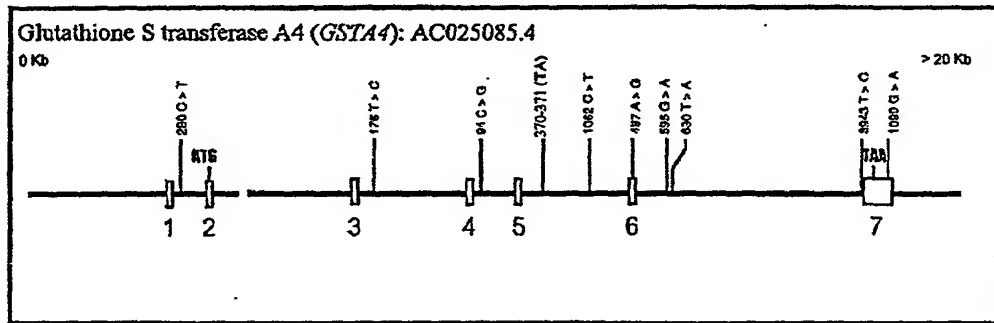


FIGURE 69

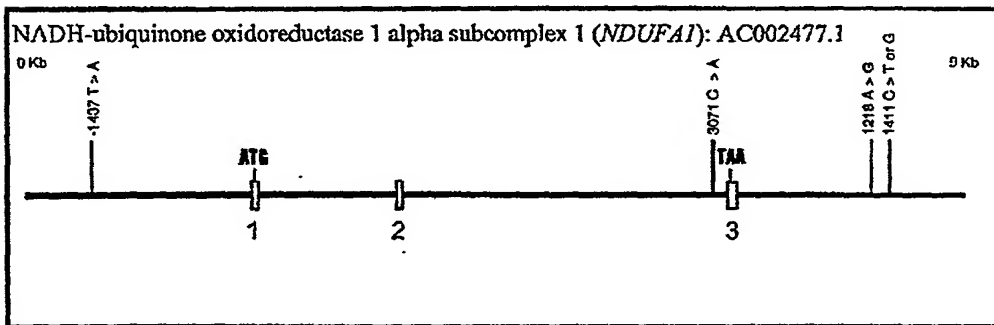


FIGURE 70

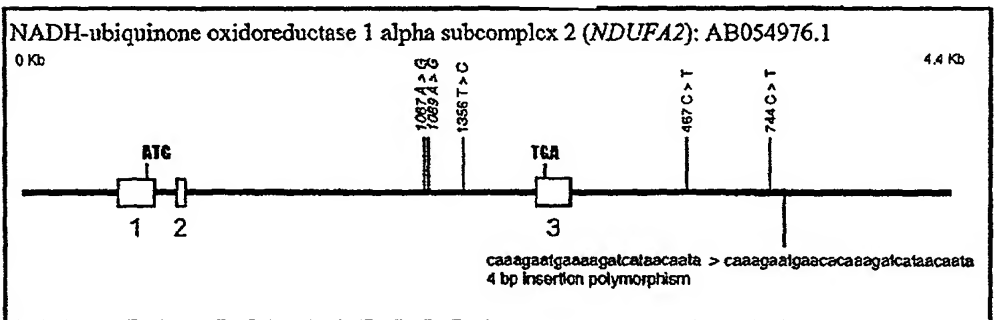


FIGURE 71

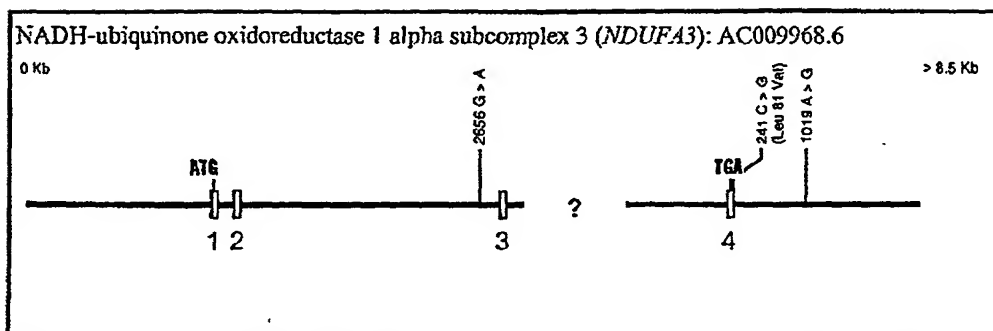


FIGURE 72

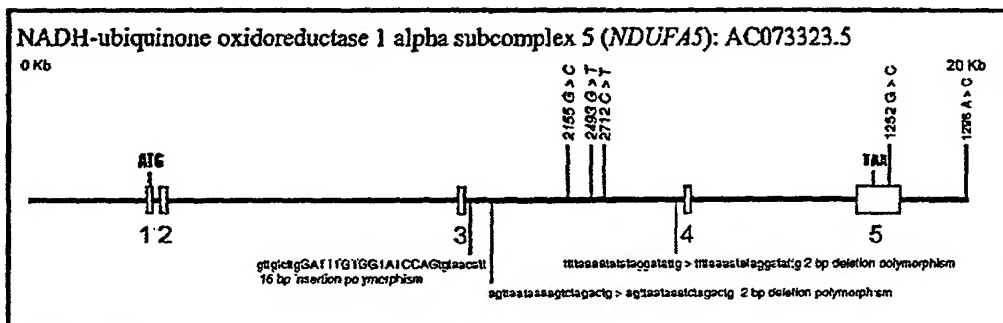


FIGURE 73

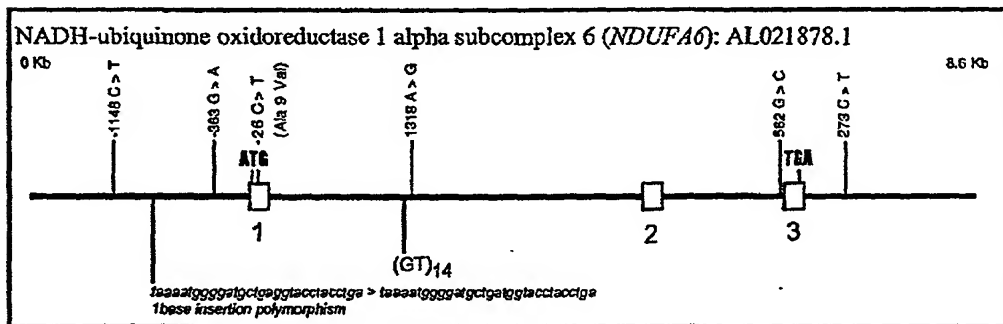
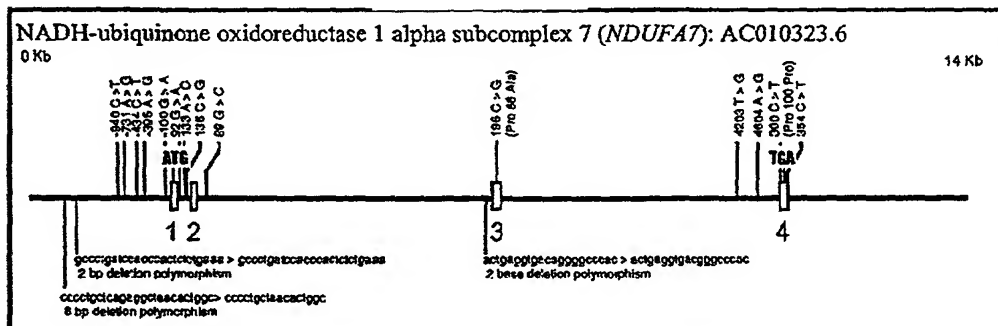


FIGURE 74



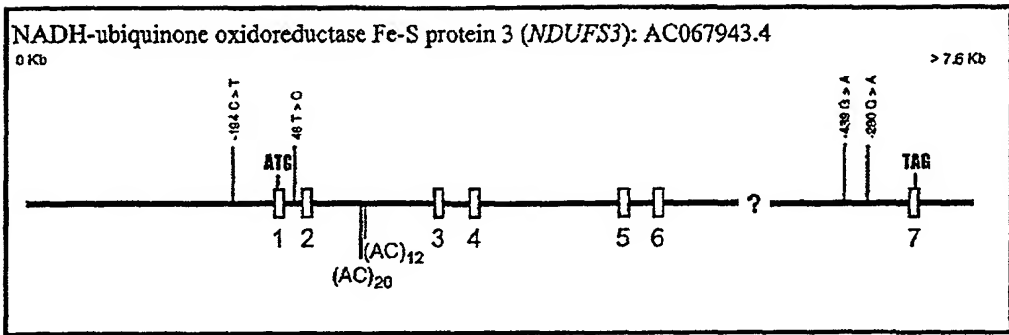
[illegible]

FIGURE 80

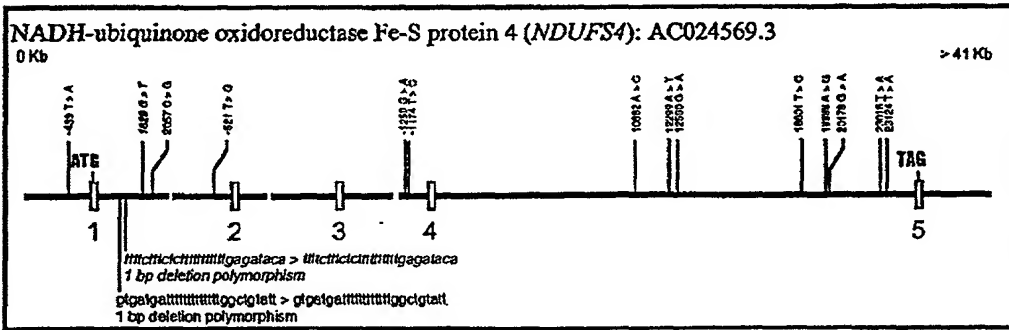


FIGURE 81

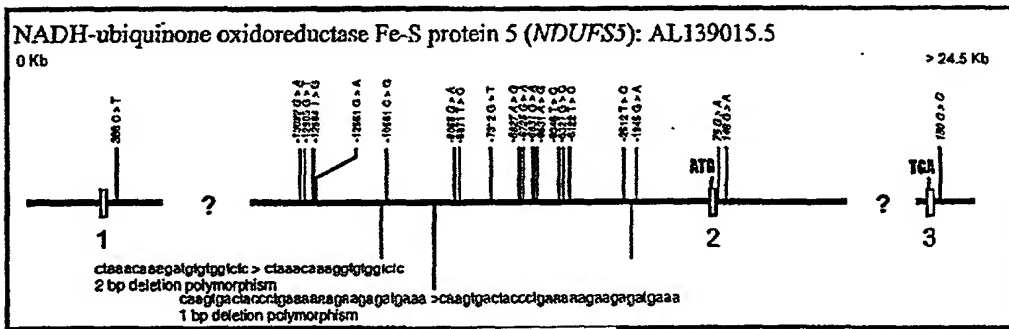
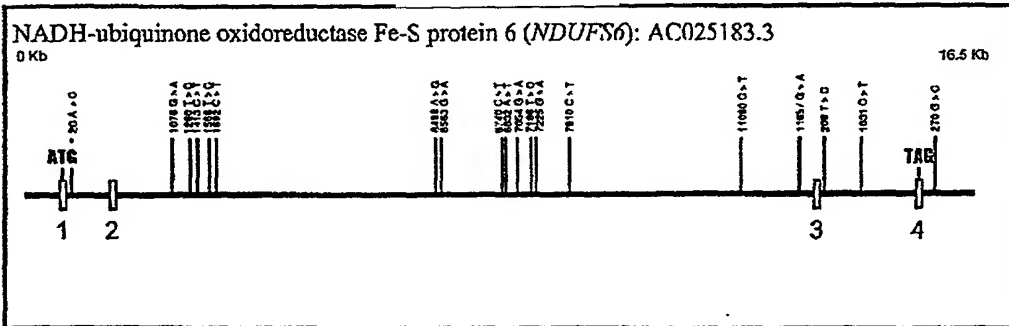


FIGURE 82



FOUO "SECRET"

SNP Information for IMS-JST104917

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST104917
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGEASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Keyword

Search

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	806730	12	4625643

Gene Information

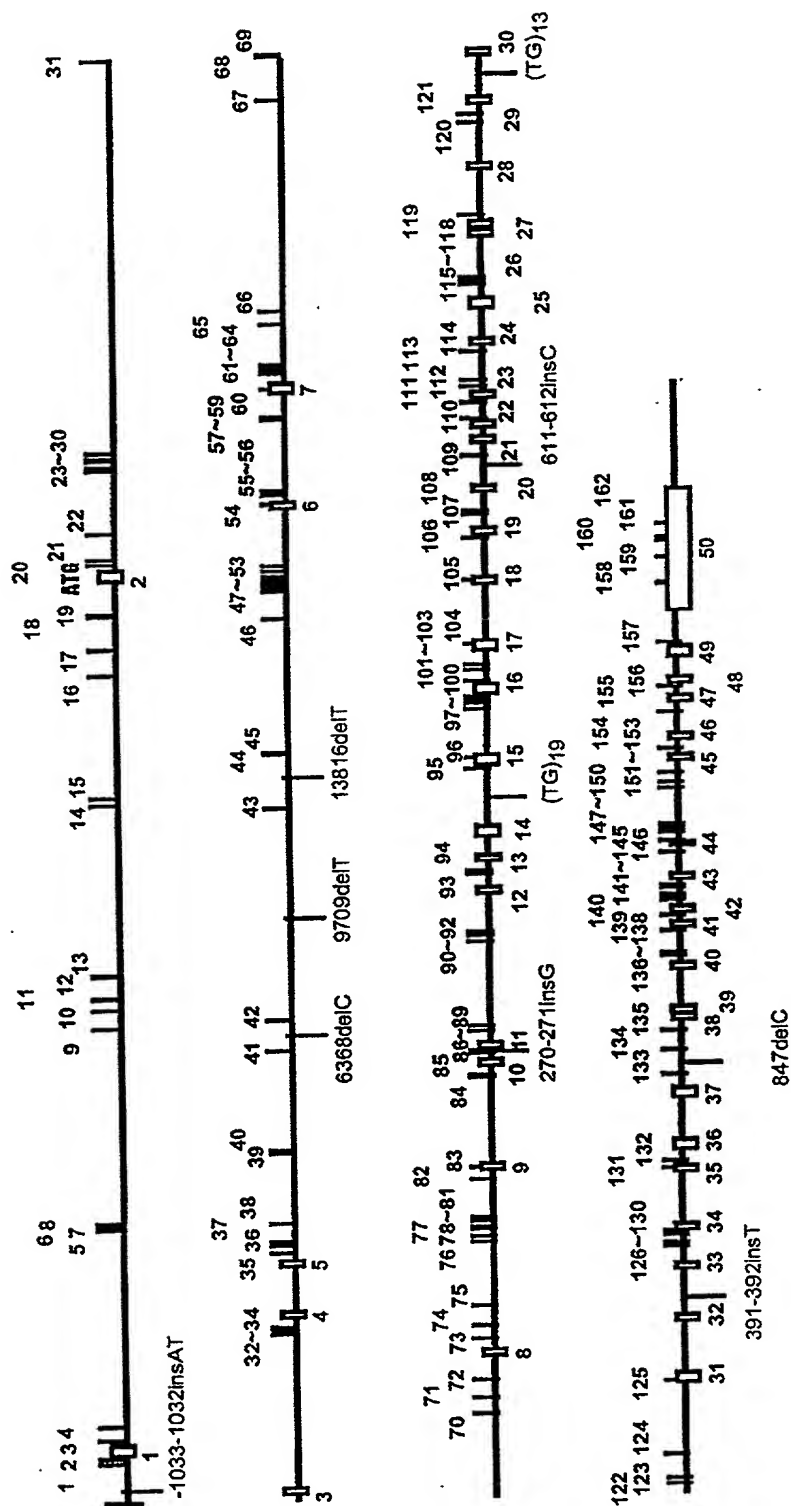
Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	

FIGURE 87

SNPs

ABCA1 ACCESSION AF275948.1



Catechol-O-methyltransferase (COMT)

ACCESSION AC000080

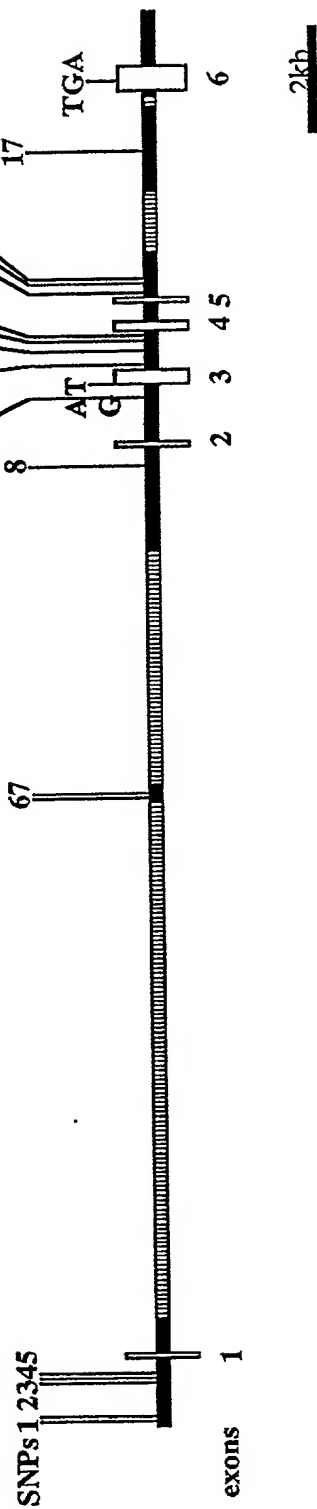
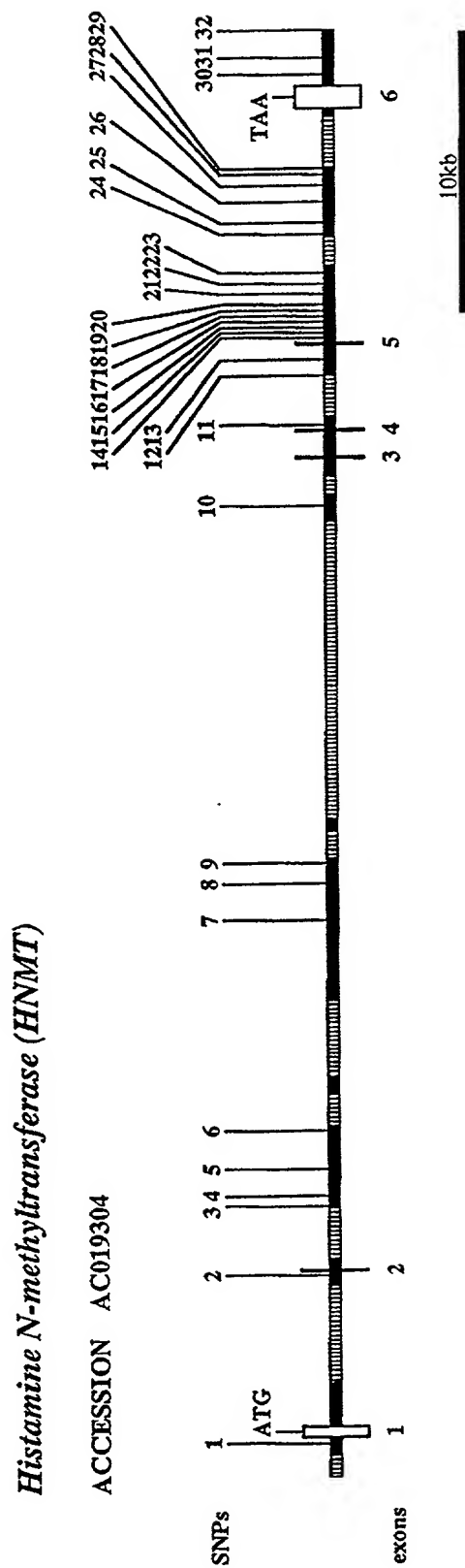


FIGURE 88

FIGURE 89



Cytochrome P450, subfamily I, polypeptide 1 (CYP1A1)

ACCESSION X04300

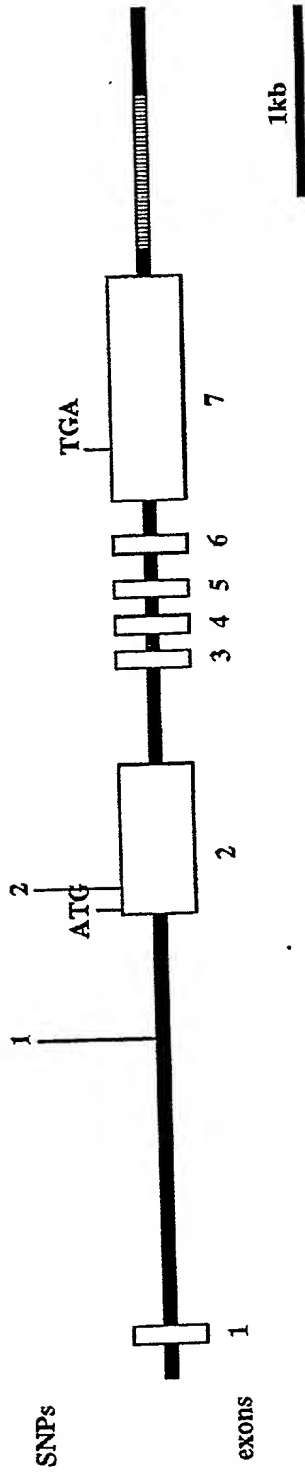


FIGURE 90

Cytochrome P450, subfamily 1, polypeptide 2 (CYP1A2)

ACCESSION AC020705

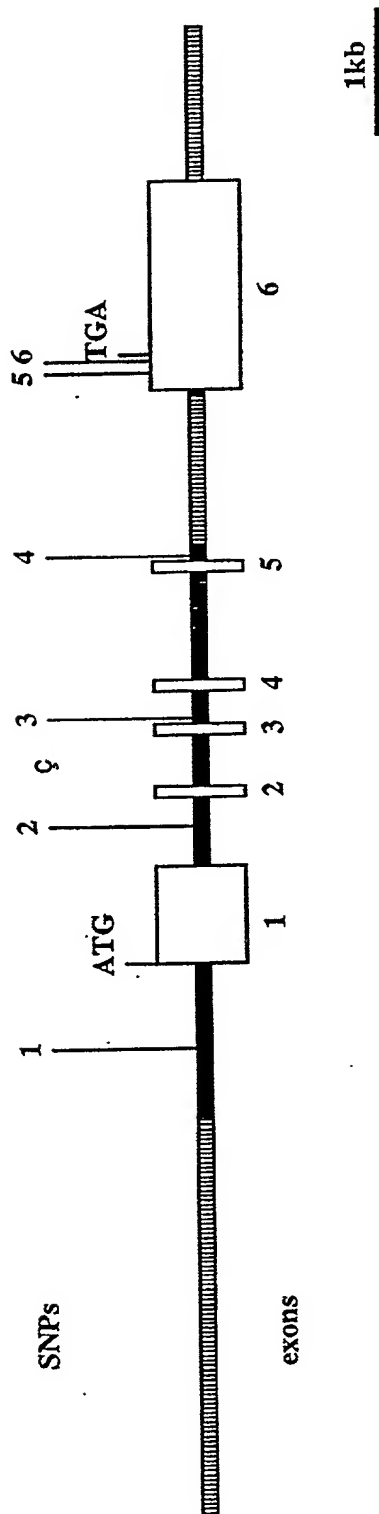


FIGURE 91

Cytochrome P450, subfamily I, polypeptide 1 (CYP1B1)

ACCESSION AC009229

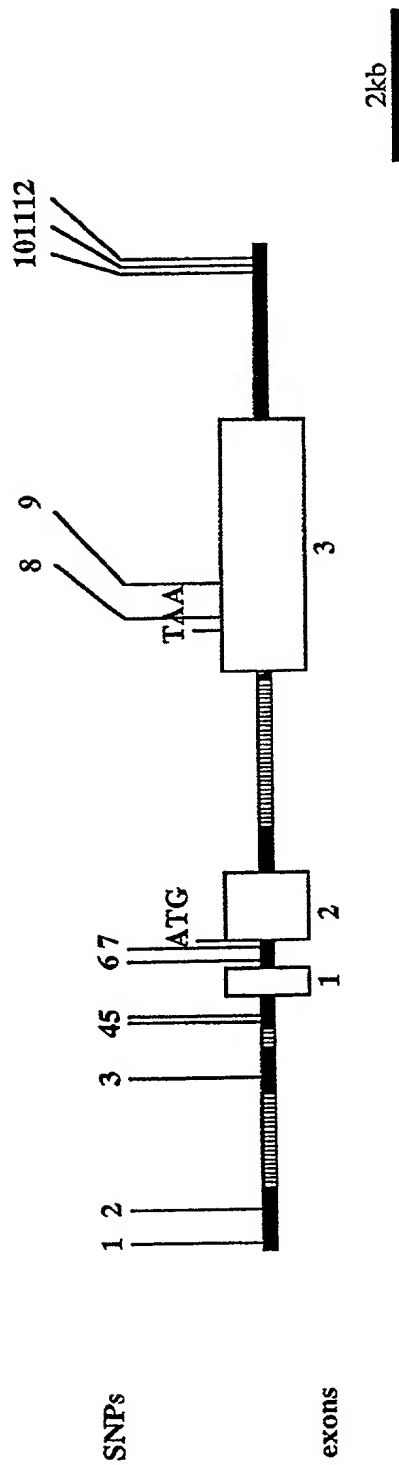


FIGURE 92

Arylacetamide deacetylase (AADAC)

ACCESSION AC068647

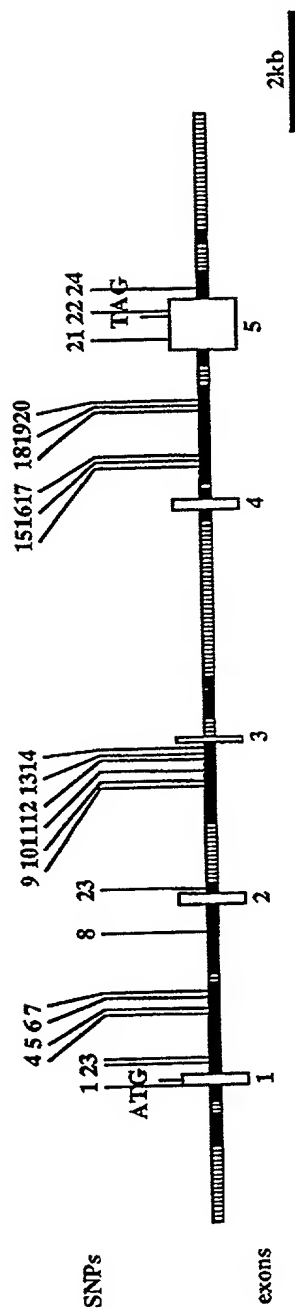
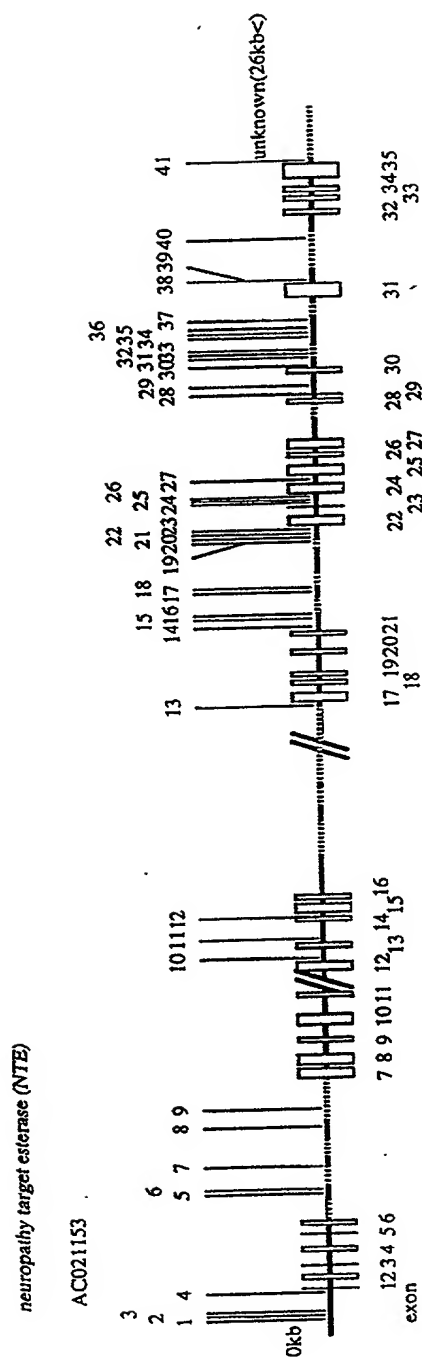


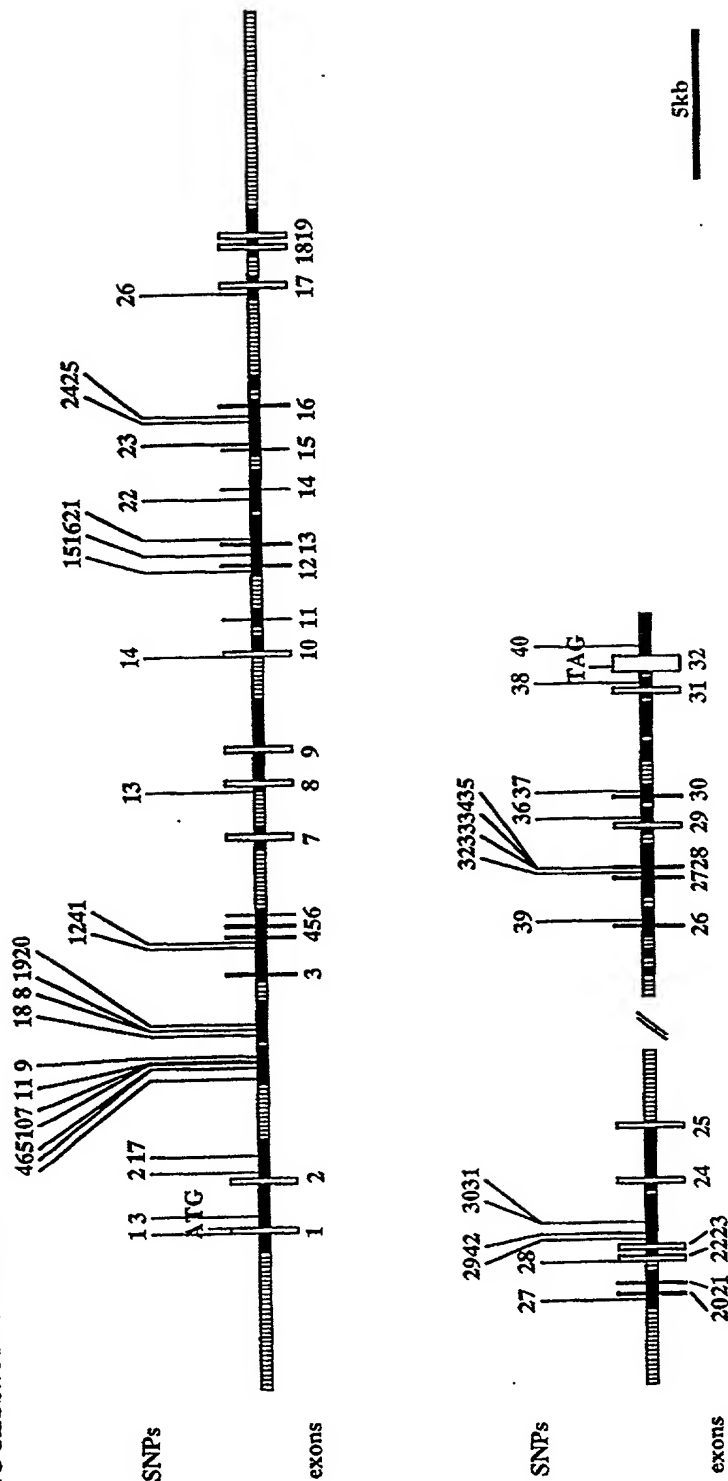
FIGURE 93

FIGURE 94



ATP-binding cassette, sub-family C (CFTR/MRP), member2 (MRP2)

ACCESSION AL392107



NT_022171.2

Observed : C/T
 3' Assay : CTCCTAGTT GCGGGAGTA GCGGGAAGAG CCTTCCTCGC GTTAATTATG CAATAAGAAAG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 (Graphical View of this Entry)
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 526155 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_022171.2.20010209_1
 Amplified region : 525548..526488 in NT_022171
 size : 941

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TTTTCCTGGAT GGAGGCCAG C	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075522

12/17/2001

FIGURE 97

ATP-binding cassette, sub-family B, member 3 (ABCB3)
ACCESSION X66401

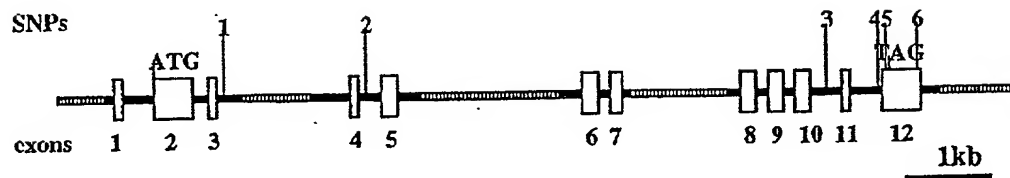


FIGURE 98

ATP-binding cassette, sub-family B, member 7 (ABCB7)
ACCESSION AL360179

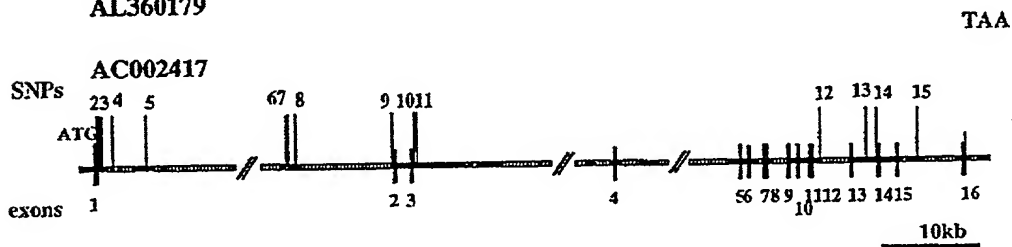
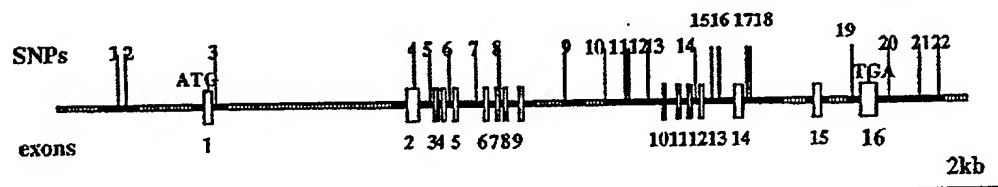


FIGURE 99

ATP-binding cassette, sub-family B, member 8 (ABCB8)
ACCESSION AC010973



NT_006124.3 "CEB3E00T"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TGGCGCGGT GGCTCAGCC TGTAATCCA GCACTTGGG AGGCCGAGGT GGGCGGATCA
Observed : T/C
3' Assay : GAGTCAGGA GATCGAGACC ACGATGAAC CCGTCTCTA CTAAATATC AAAAAATTAG
Comment : repeat sequence (SNP is present in repeat sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_006124.3 (Graphical View of this Entry)
Chromosome : 4
map
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
Position in Sequence : 468642 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006124.3 20010416_6
Amplified region : 467851..468999 in NT_006124
size : 1149
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

FIGURE 102

ATP-binding cassette, sub-family B, member 11 (ABCB11)

ACCESSION AC008177
AC069137

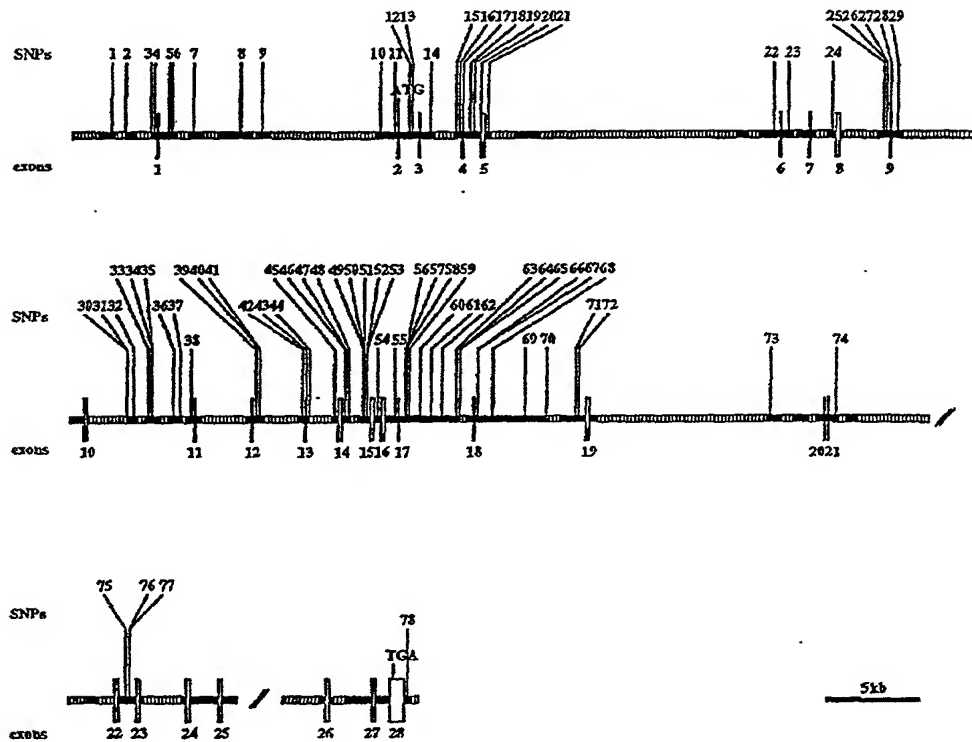


FIGURE 103

Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)

ACCESSION AL356793

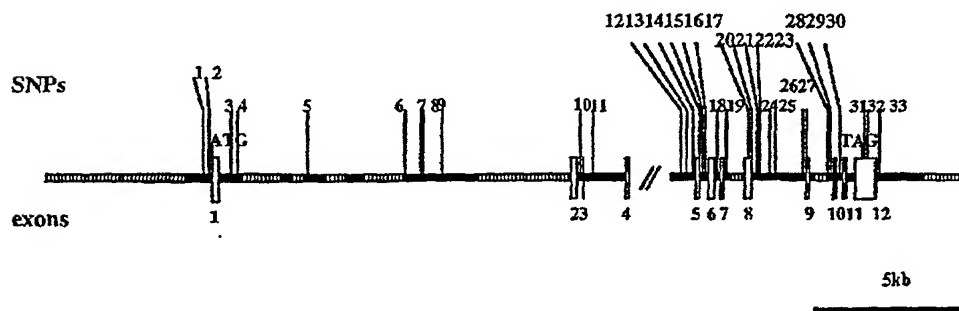


FIGURE 104

Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)

ACCESSION AC009974

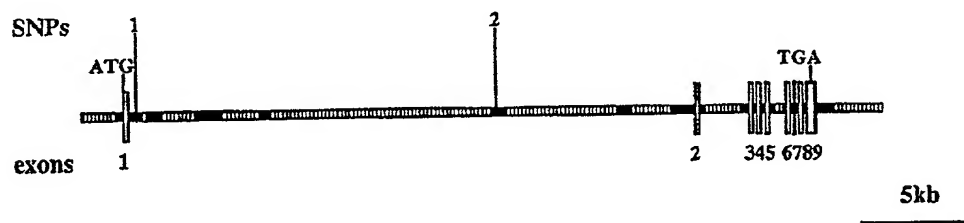


FIGURE 105

Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2)

ACCESSION AC005336

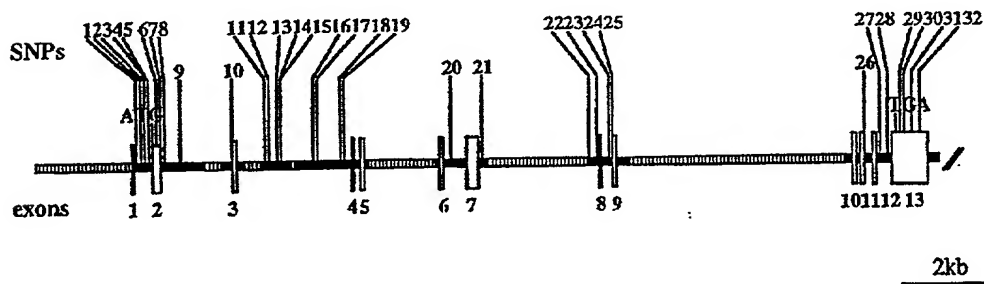


FIGURE 106

Cytochrome P450, subfamily 4F, polypeptide 3 (CYP4F3)

ACCESSION AD000685

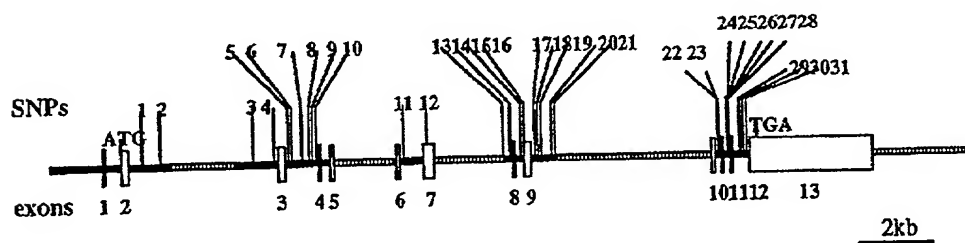


FIGURE 107

Cytochrome P450, subfamily 4F, polypeptide 8 (CYP4F8)

ACCESSION AC068845

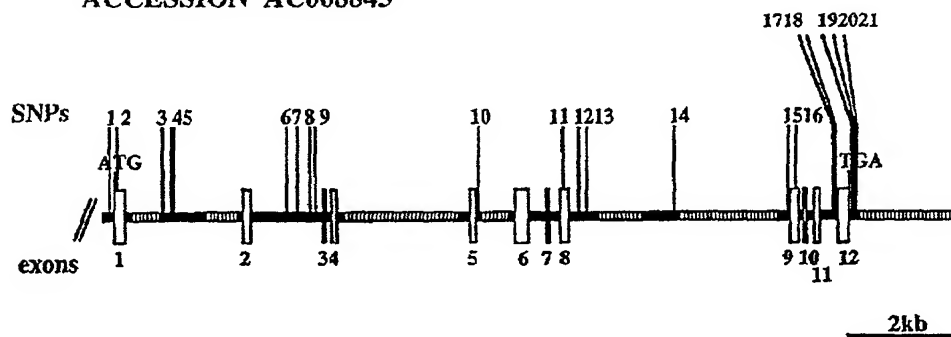


FIGURE 108

Aldehyde dehydrogenase 1 (ALDH1)

ACCESSION

AC009284

AL162416

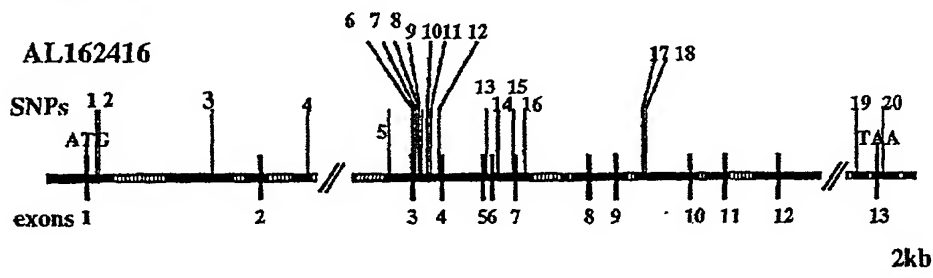


FIGURE 109

Aldehyde dehydrogenase 2 (ALDH2)

ACCESSION AC002996

AC003029

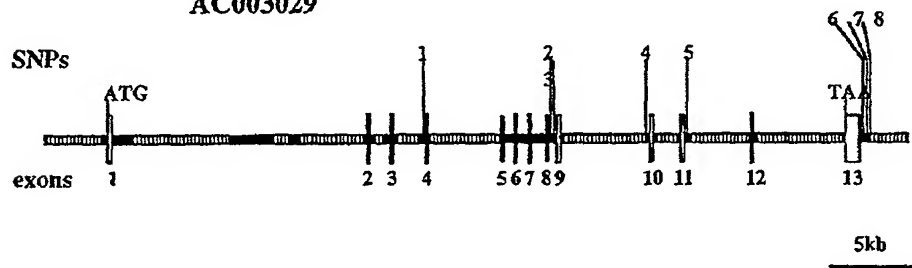


FIGURE 110

Aldehyde dehydrogenase 7 (ALDH7)

ACCESSION AC004923

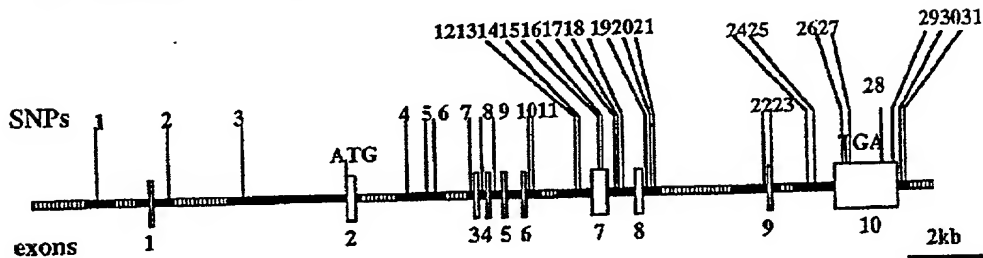


FIGURE 111

Aldehyde dehydrogenase 8 (ALDH8)

ACCESSION AC021987

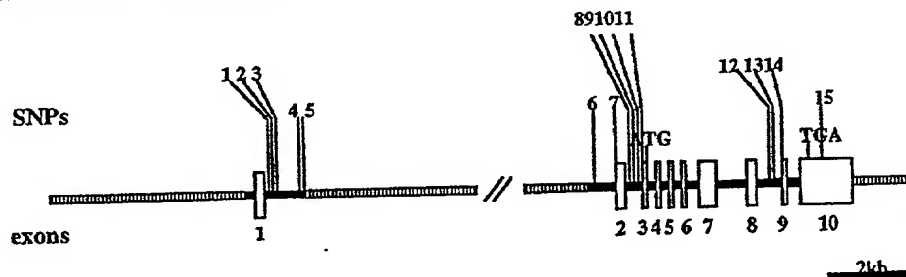


FIGURE 112

Aldehyde dehydrogenase 9 (ALDH9)

ACCESSION AL451074

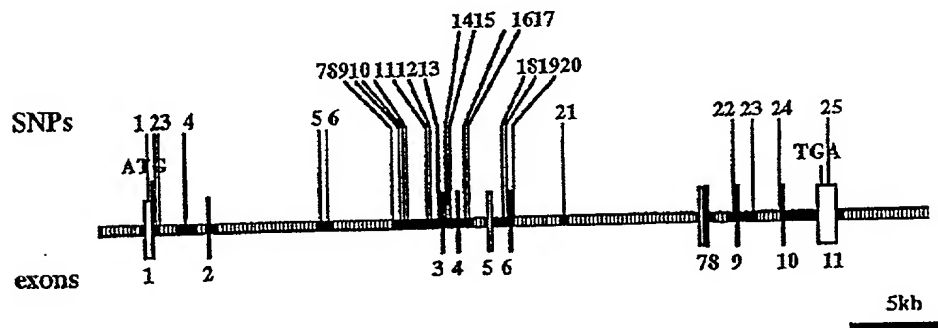


FIGURE 113

Aldehyde dehydrogenase 10 (ALDH10)

ACCESSION AC005722

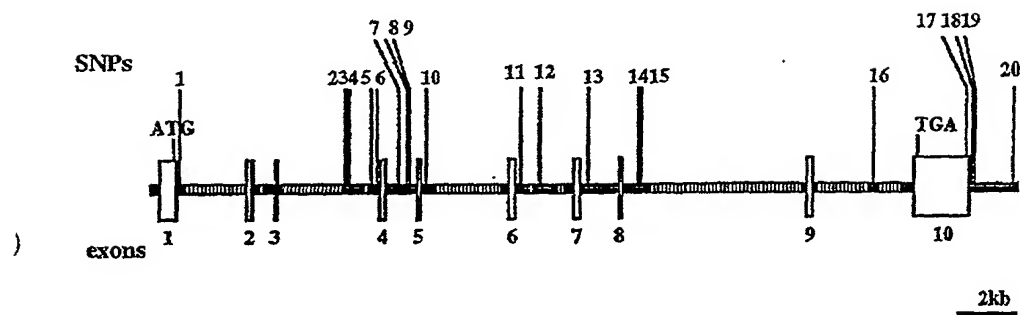


FIGURE 114

ATP binding cassette, sub-family C, member 7 (ABCC7)

ACCESSION AC000111
AC000061

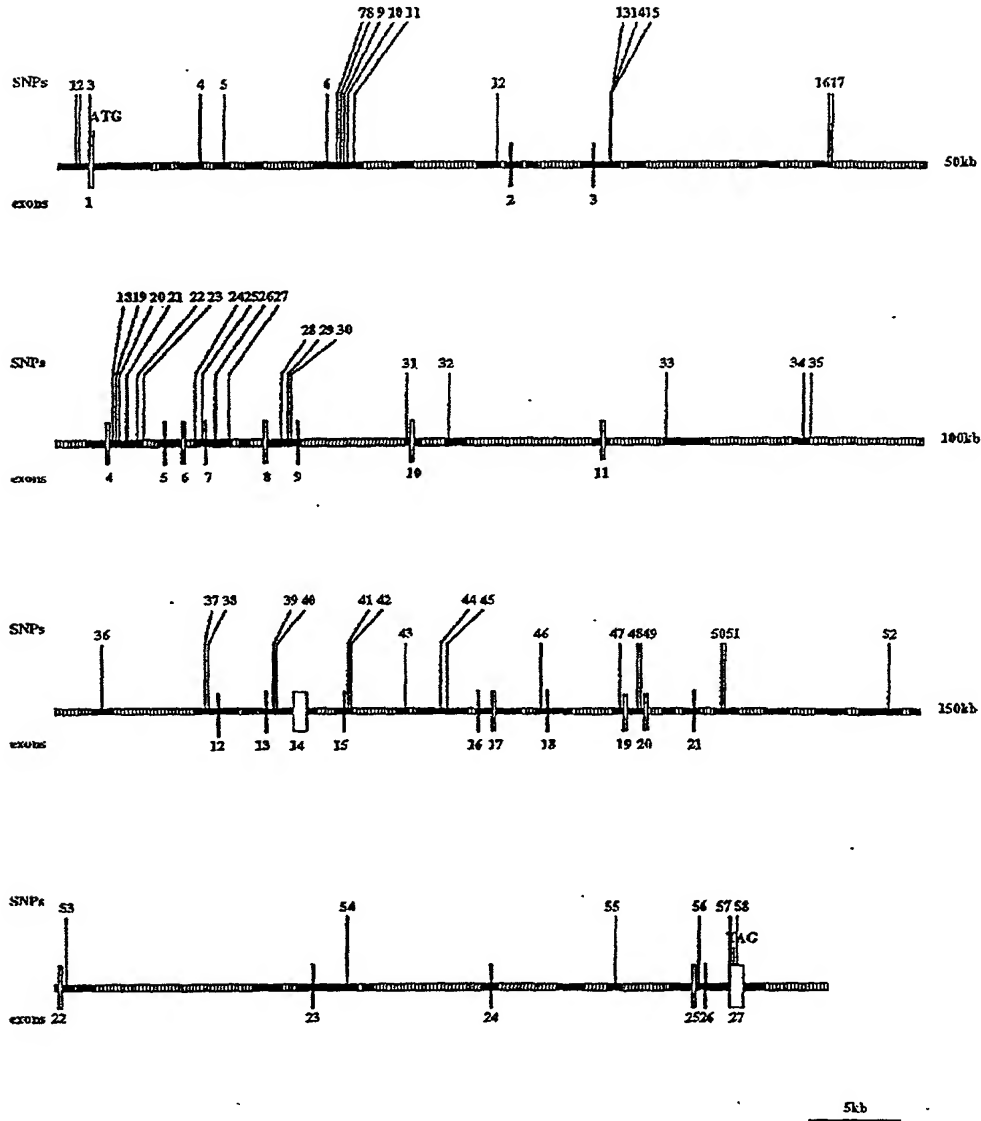


FIGURE 115

ATP binding cassette, sub-family C, member 8 (ABCC8)

ACCESSION AC000406

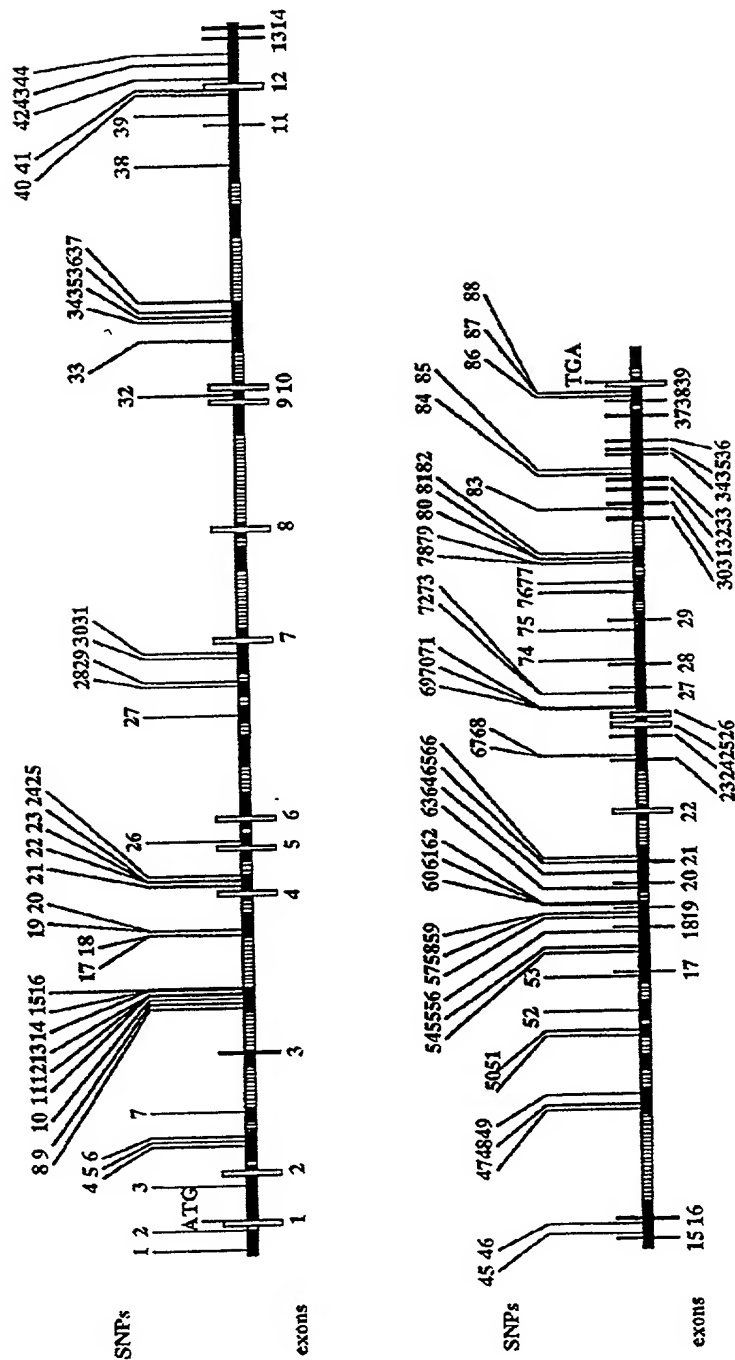
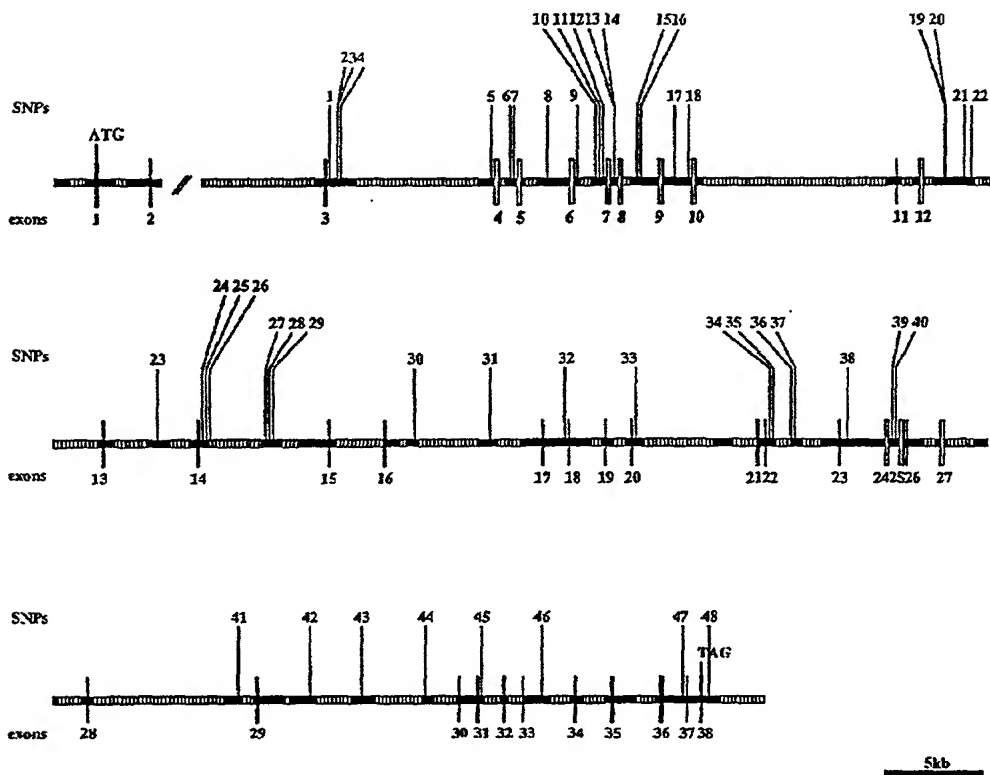


FIGURE 116

ATP binding cassette, sub-family C, member 9 (ABCC9)

ACCESSION AC084806
AC008250



Carboxylesterase 1 (CES1)

ACCESSION AC007602

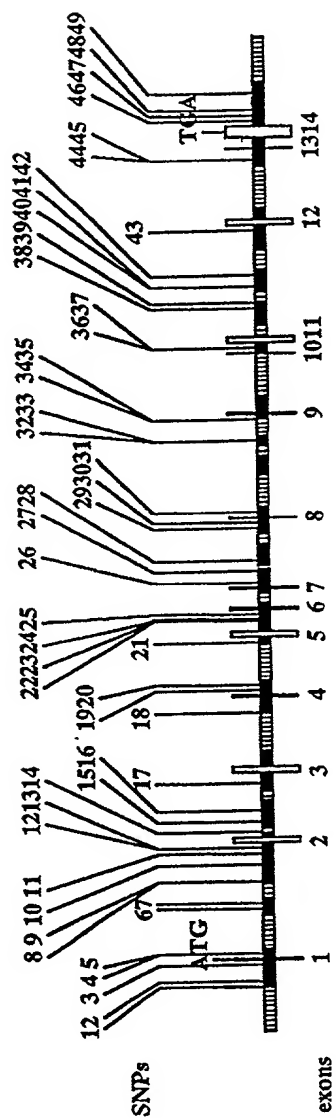


FIGURE 117

FIGURE 118

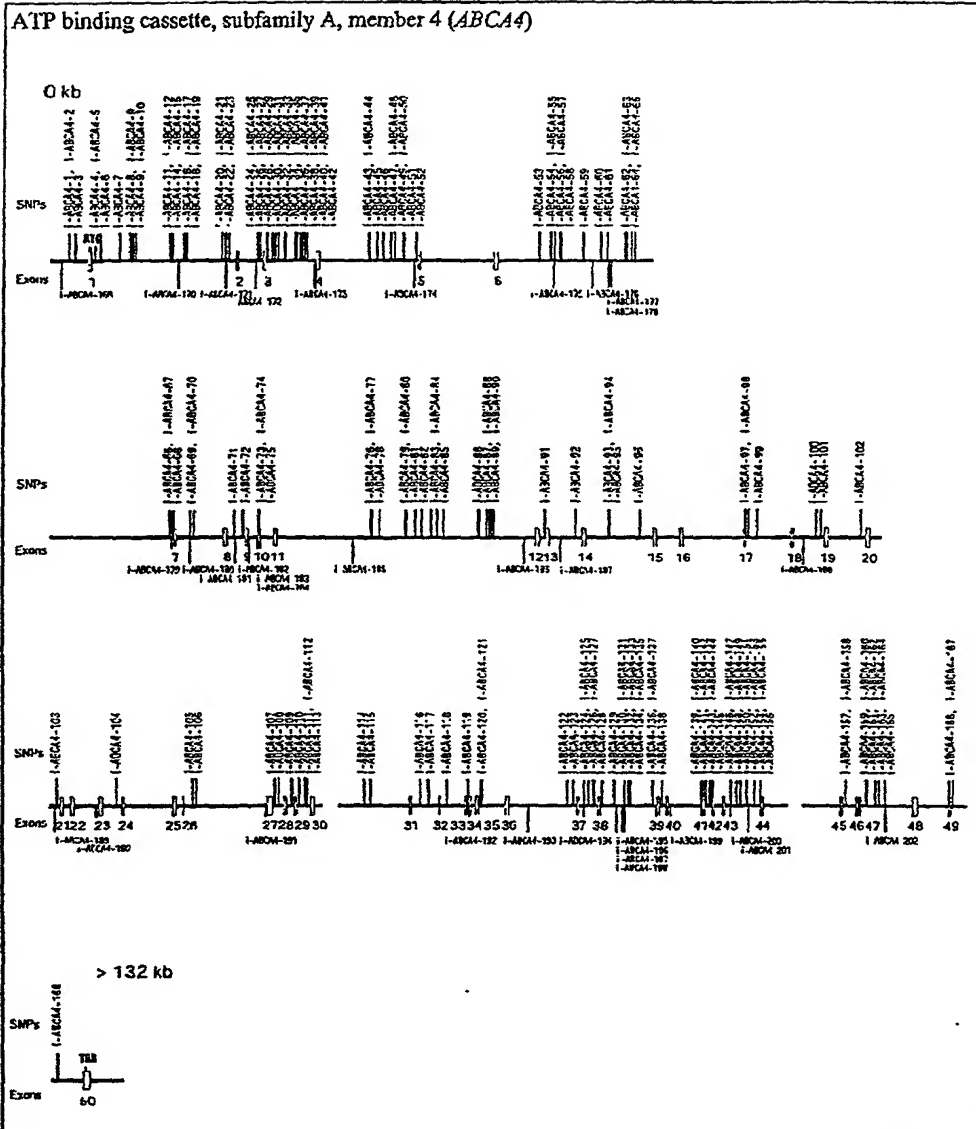


FIGURE 119

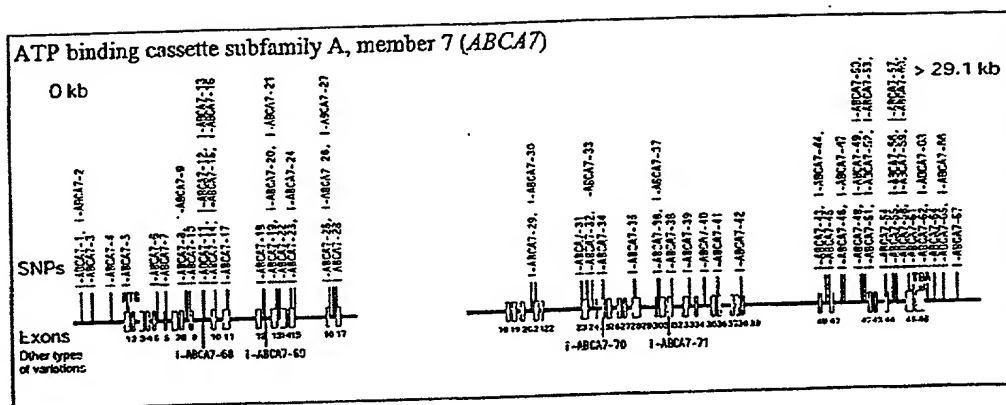


FIGURE 120

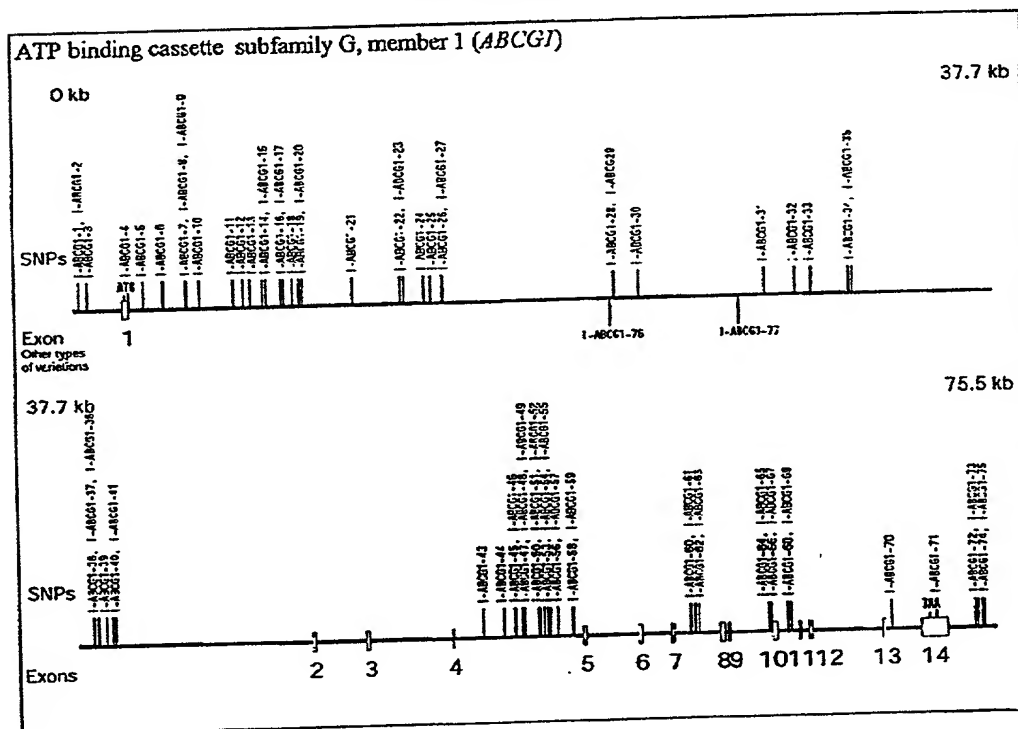


FIGURE 121

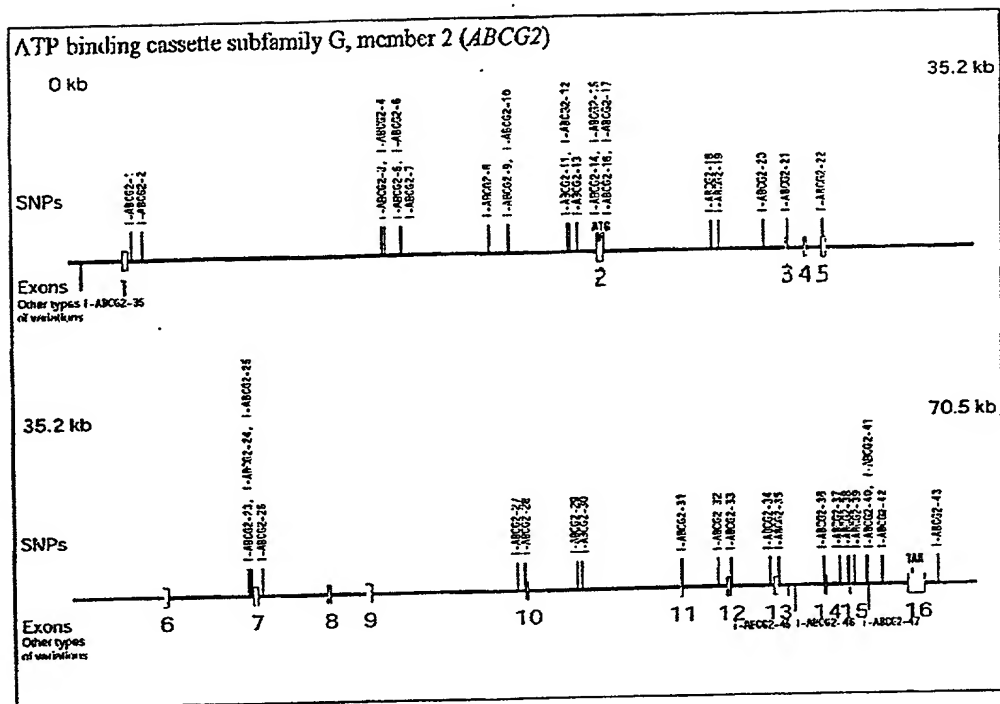


FIGURE 122

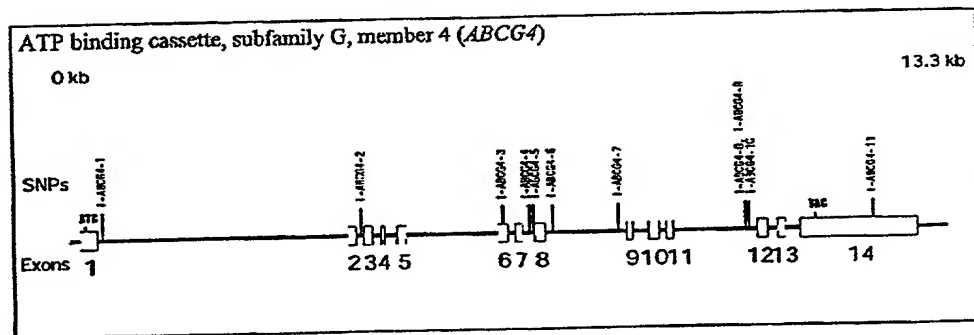


FIGURE 123

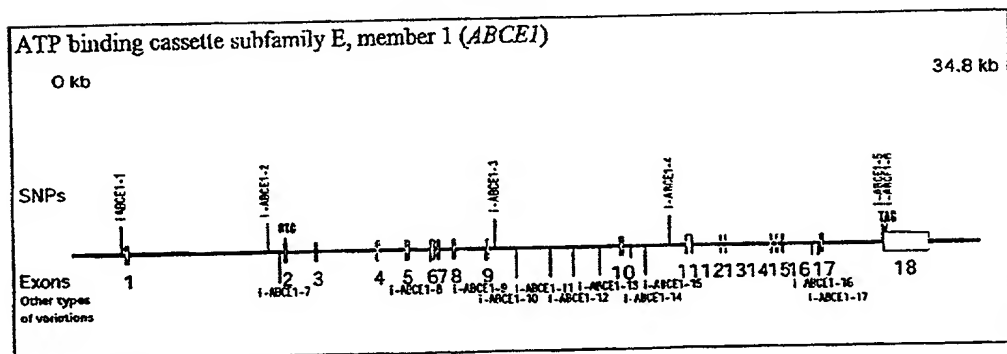


FIGURE 124

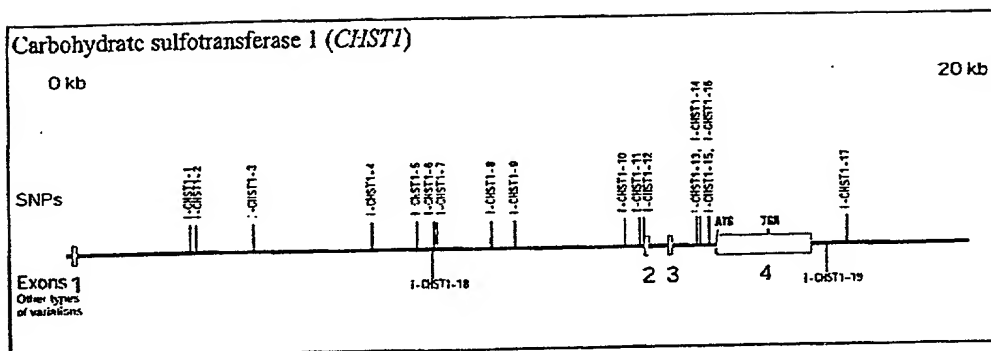


FIGURE 125

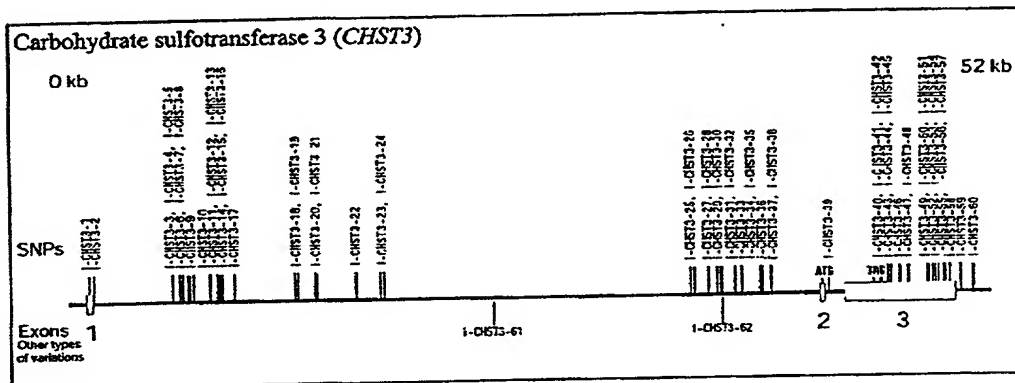


FIGURE 126

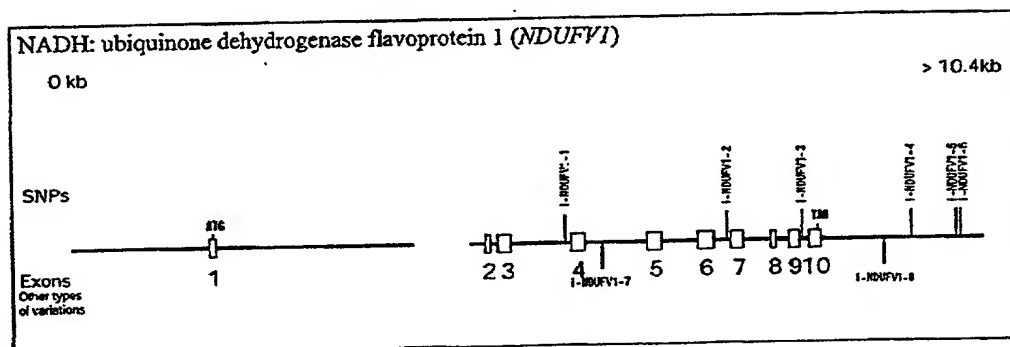


FIGURE 127

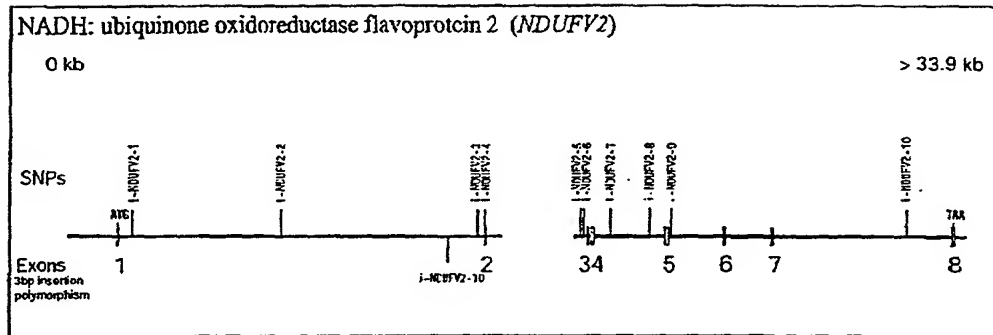


FIGURE 128

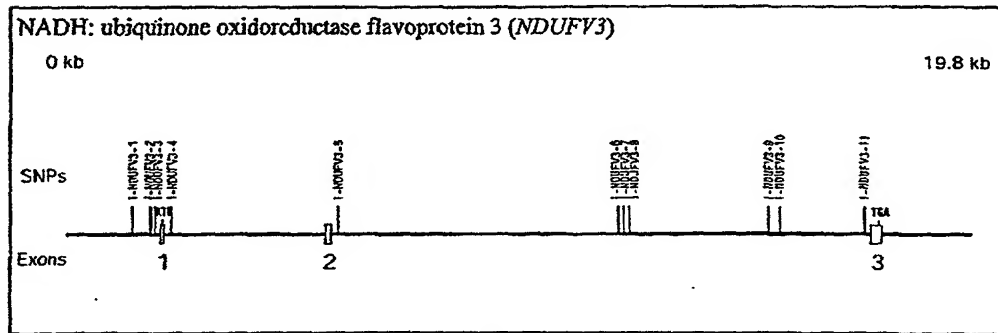


FIGURE 129

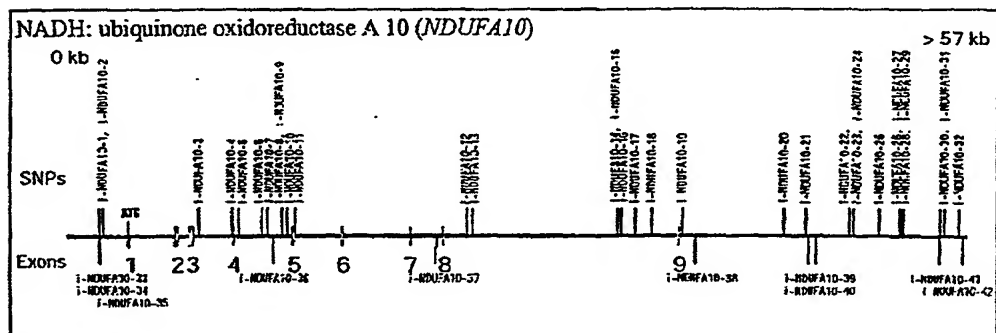


FIGURE 130

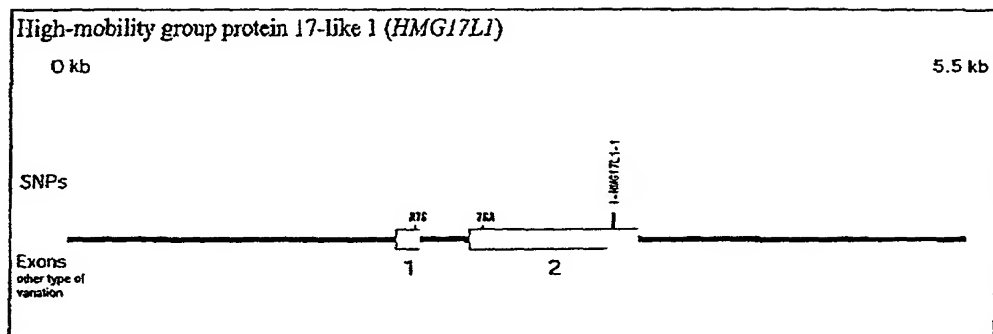


FIGURE 131

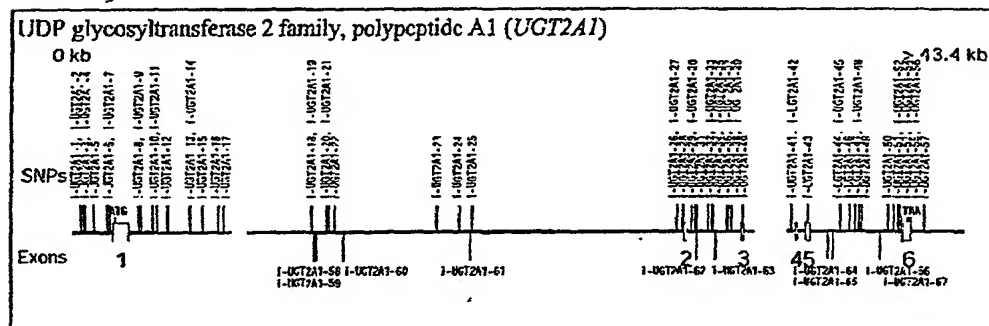


FIGURE 132

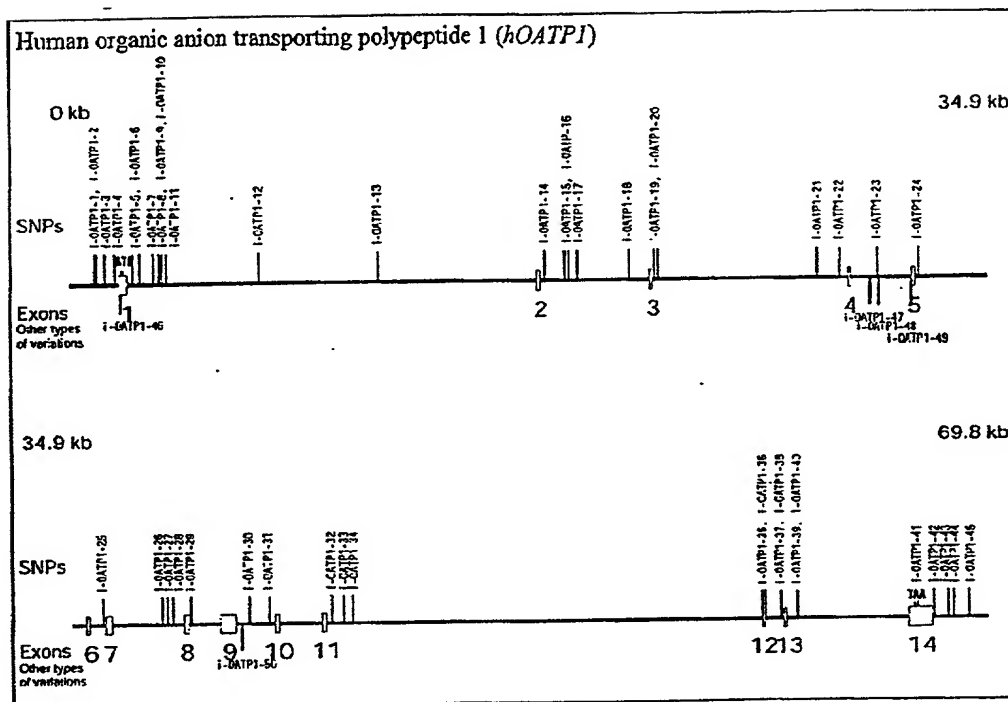


FIGURE 134

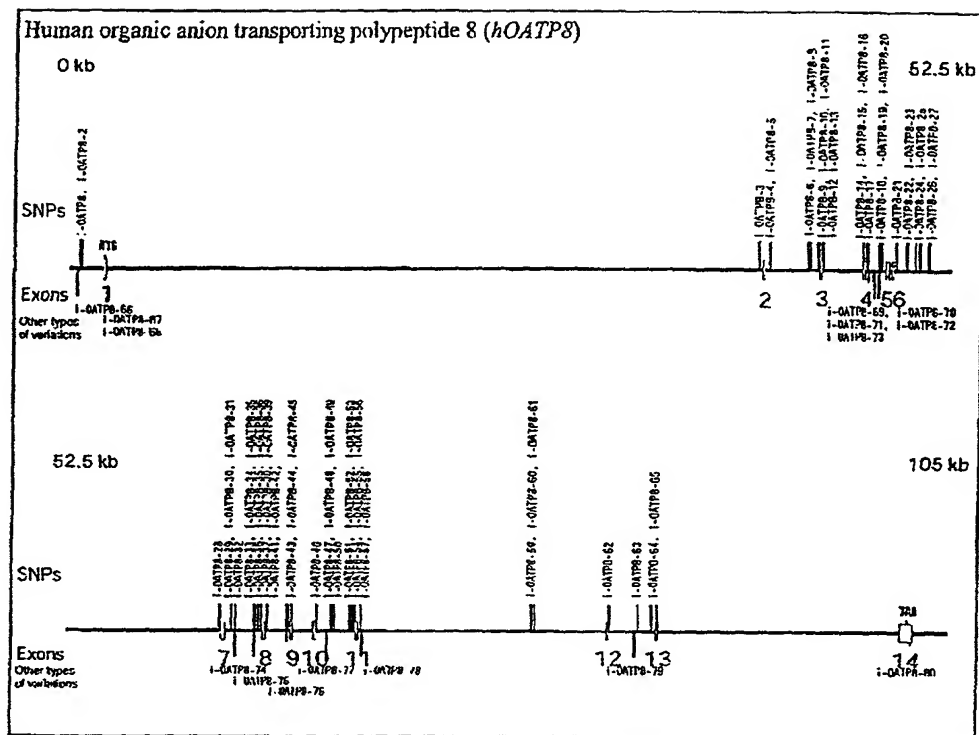


FIGURE 135

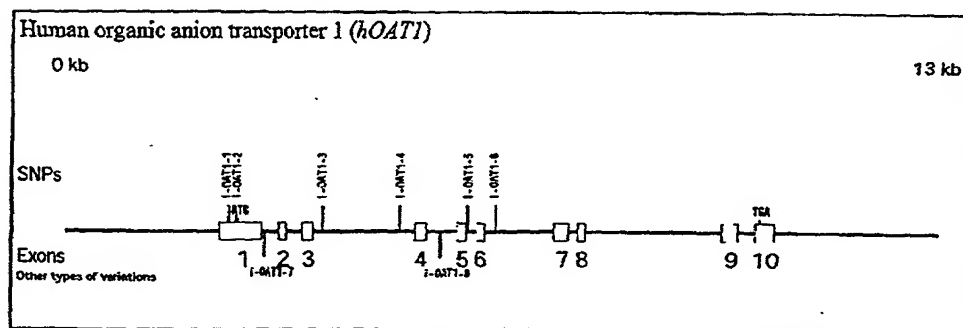


FIGURE 136

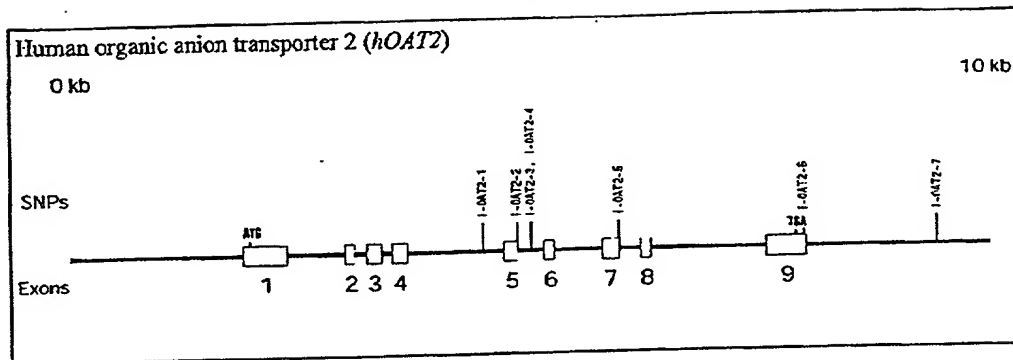
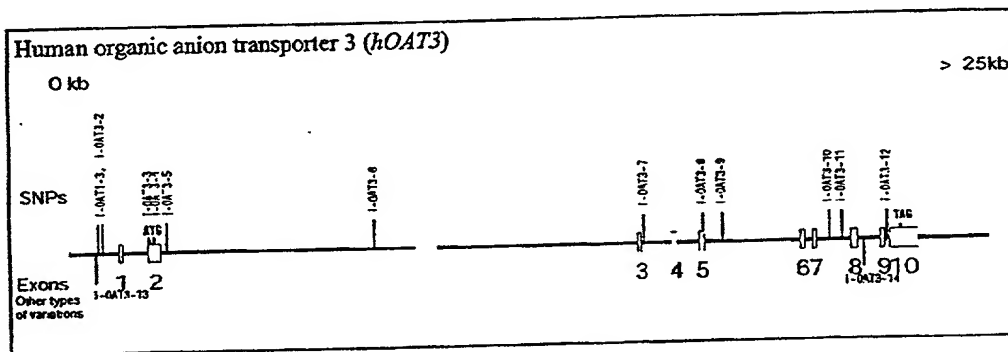


FIGURE 137



Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2) ACCESSION AC025431
AC012653

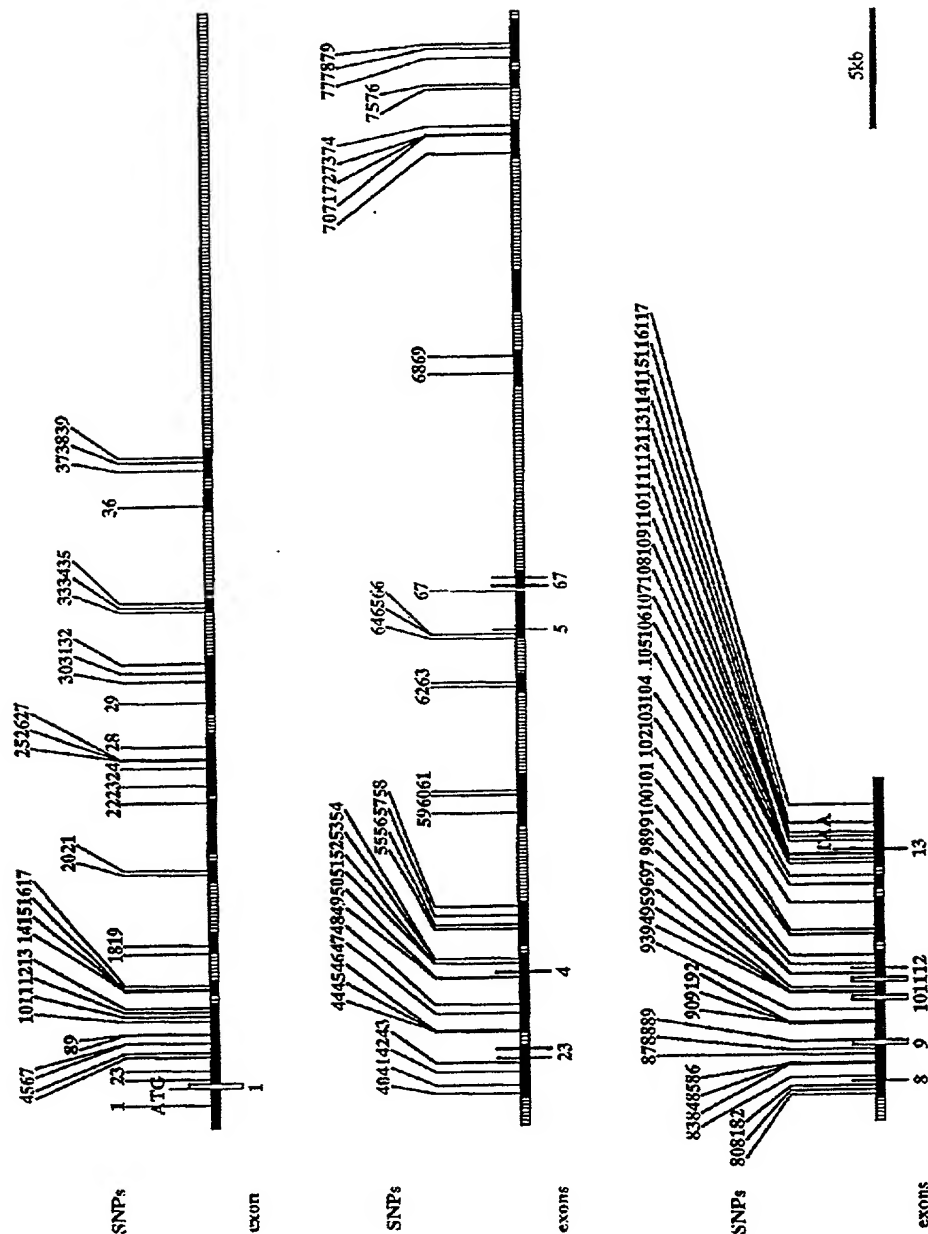


FIGURE 138

Aldehyde dehydrogenase 1 family, member A3 (ALDH1A3)

ACCESSION AC015712

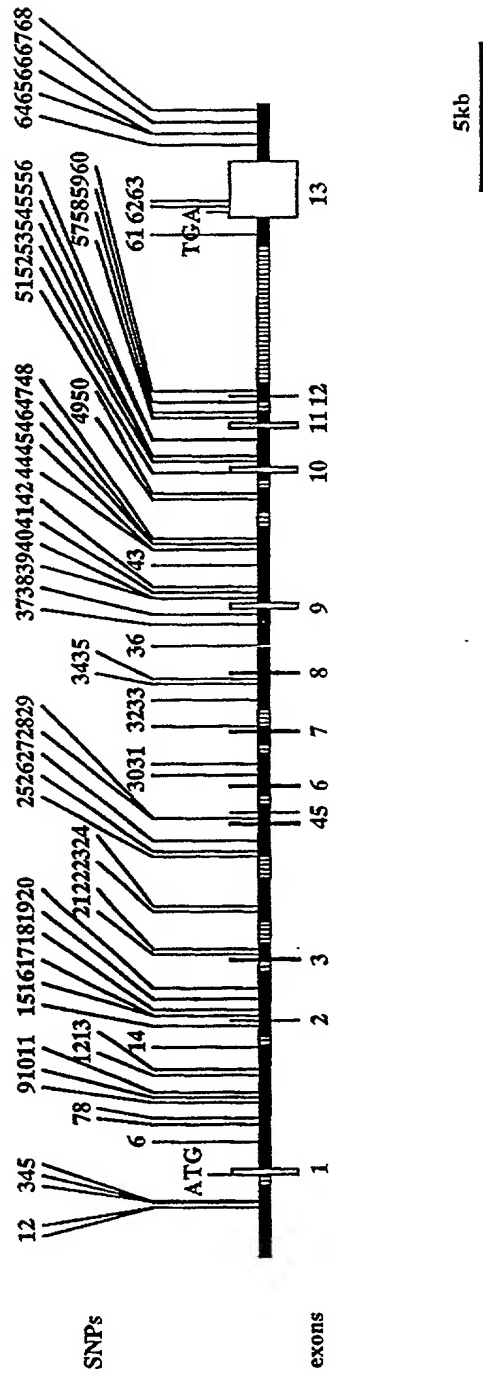
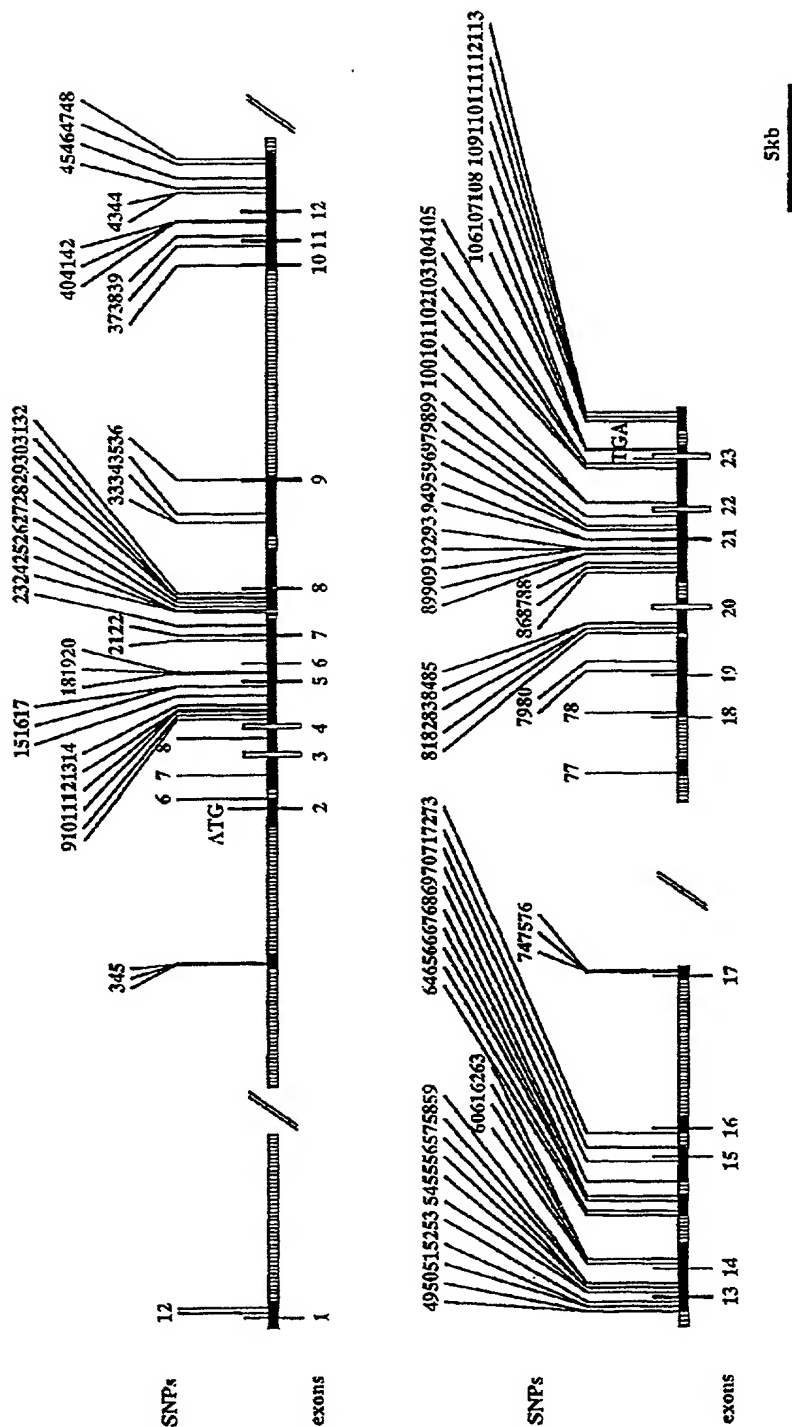


FIGURE 140

Formyltetrahydrofolate dehydrogenase (FTHFD /ALDH1L1)

ACCESSION AC079848



Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)

ACCESSION AF280107

FIGURE 141

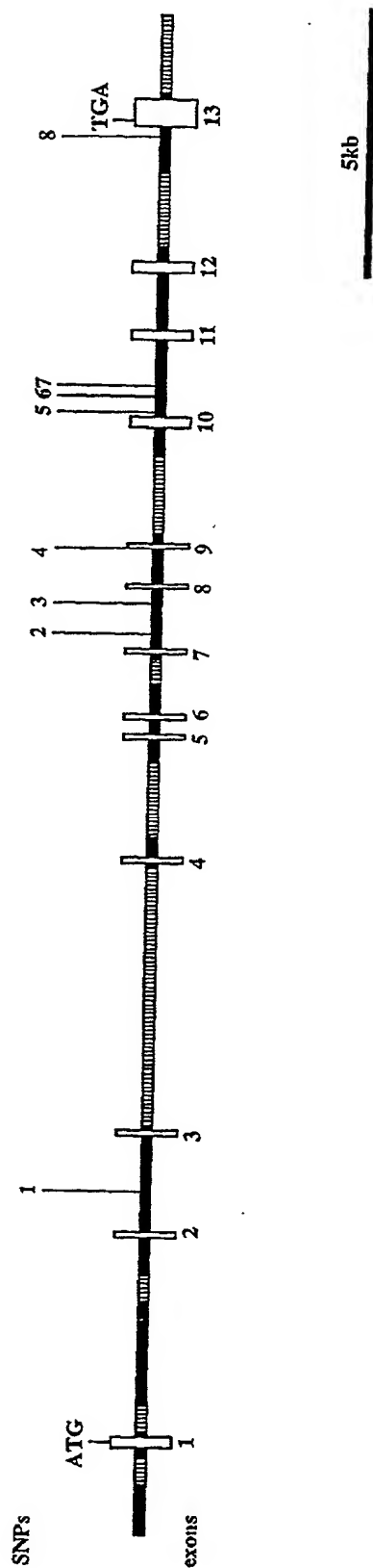
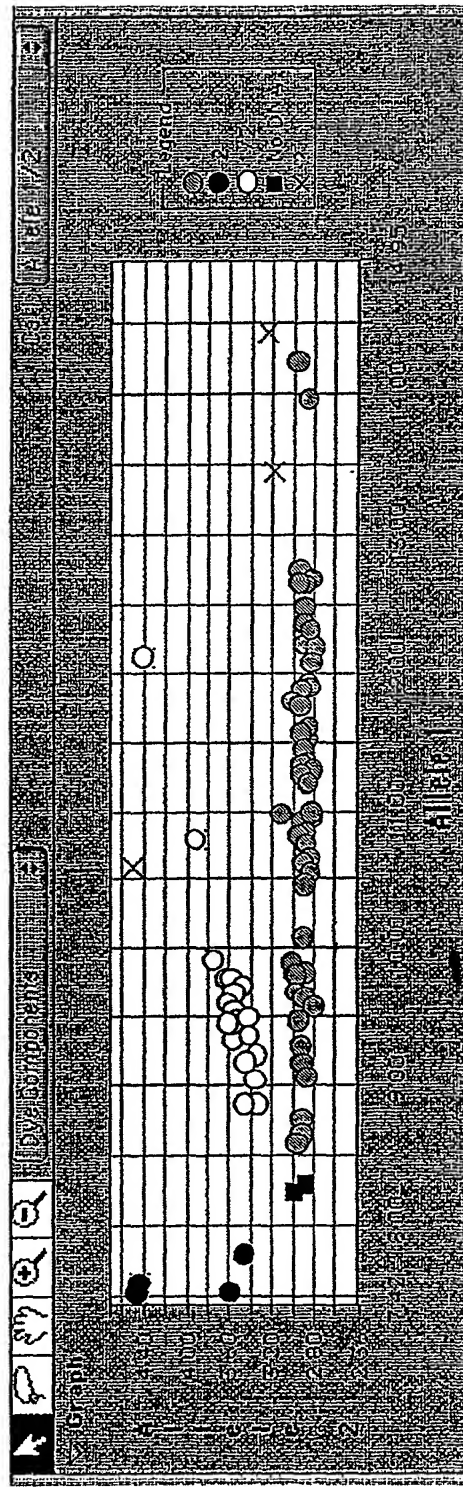
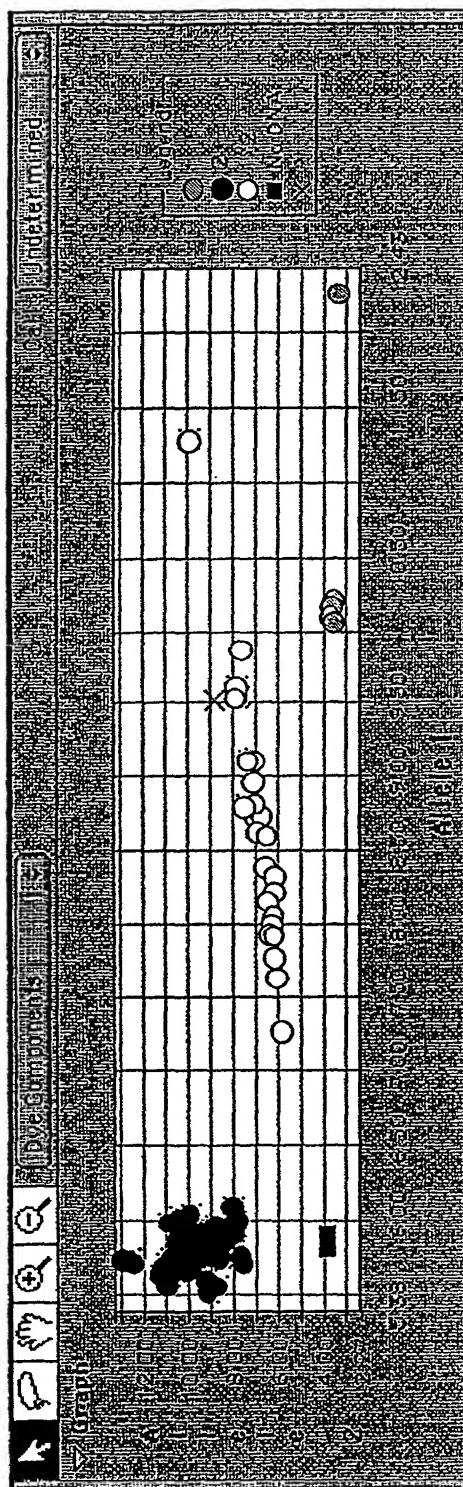


FIGURE 142



NO	GENE	LONG_GENE_NAME	CHROM.	REF. MRNA	L-LINK	OMIM_ID	EXONS	NO GENE
1	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	1
2	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	2
3	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	3
4	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	4
5	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	5
6	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	6
7	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	7
8	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	8
9	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	9
10	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	10
11	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	11
12	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	12
13	TAP2	transporter 2, ATP-binding cassette, sub-family	chr6	NM_000544	6891	170261	12	13
14	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	1
15	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	2
16	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	3
17	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	4
18	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	5
19	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	6
20	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	7
21	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	8
22	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	9
23	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	10
24	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	11
25	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	12
26	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	13
27	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	14
28	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	15
29	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	16
30	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	17
31	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	18
32	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	19
33	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	20
34	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	21
35	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	22
36	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	23

37	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	24
38	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	25
39	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	26
40	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	27
41	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	28
42	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	29
43	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	30
44	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	31
45	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	32
47	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	1
48	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	2
49	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	3
50	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	4
51	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	5
52	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	6
53	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	7
54	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	8
55	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	9
56	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	10
57	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	11
58	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	12
59	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	13
60	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	14
61	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	15
62	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	16
63	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	chr1	NM_000120	2052	132810	9	17
66	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	2
67	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	3
68	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	4
69	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	5
70	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	6
71	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	7
72	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	8
73	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	9
74	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	10
75	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	11
76	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	12

77	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	13
78	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	14
79	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	15
80	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	16
81	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	17
82	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	18
83	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	19
84	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	20
85	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	21
86	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	22
87	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	23
88	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	24
89	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	25
90	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	26
91	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	27
92	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	28
93	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	29
94	EPHX2	epoxide hydrolase 2, cytoplasmic	chr8	NM_001979	2053	132811	19	30
95	GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	1
96	GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	2
97	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	1
98	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	2
99	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	3
100	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	4
101	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	5
102	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	6
103	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	7
104	NNMT	nicotinamide N-methyltransferase	chr11	NM_006169	4837	600008	3	8
105	NNMT	phenylethanolamine N-methyltransferase	chr17	NM_002686	5409	171190	3	1
106	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	1
107	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	2
108	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	3
109	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	4
110	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	5
111	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	6
112	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	7
113	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	8

[illegible]

[illegible]

188	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	83
189	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	84
190	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	85
191	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	8
192	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	6
193	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	87
194	PEMT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	88
195	GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	1
196	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	1
197	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	2
198	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	3
199	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	4
200	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	5
201	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	6
202	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	7
203	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	8
204	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	9
205	ALDH5	aldehyde dehydrogenase 5	chr9	NM_000692	219	100670	1	10
206	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	1
218	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	13
219	TGM1	transglutaminase 1 (K polypeptide epidermal type	chr14	NM_000359	7051	190195	16	14
221	GGT1	gamma-glutamyltransferase 1	chr22	NM_005265	2678	231950	15	
222	DIA4	NAD(P)H menadiene oxidoreductase 1,	chr16	NM_000903	1728	125860	6	1
223	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	1
224	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	2
225	PIG3	quinone oxidoreductase homolog	chr2	NM_004881	9540	605171	5	3
226	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	1
227	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	2
228	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	3
229	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	4
230	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	5
231	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	6
232	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	7
233	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	8
234	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	9
235	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	10
236	NMOR2	NAD(P)H menadiene oxidoreductase 2,	chr6	NM_000904	4835	160998	7	11

237 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	12
238 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	13
239 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	14
240 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	15
241 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	16
242 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	17
243 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	18
244 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	19
245 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	20
246 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	21
247 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	22
248 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	23
249 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	24
250 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	25
251 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	26
252 NMOR2	NAD(P)H menadione oxidoreductase 2,	chr6	NM_000904	4835	160998	7	27
253 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	1
254 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	2
255 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	3
256 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	4
257 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	5
258 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	6
259 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	7
260 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	8
261 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	9
262 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	10
263 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	11
264 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	12
265 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	13
266 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	14
267 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	15
268 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	16
269 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	17
270 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	18
271 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	19
272 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	20
273 SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	21

274	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	22
275	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	23
276	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	24
277	SULT1A1	sulfotransferase family, cytosolic, 1A,	chr16	NM_001055	6817	171150	7	25
278	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	1
279	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	2
280	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	3
281	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	4
282	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	5
283	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	6
284	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	7
285	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	8
286	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	9
287	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	10
288	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	11
289	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	12
290	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	13
291	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	14
292	SULT1A2	sulfotransferase family, cytosolic, 1A,	chr16	NM_001054	6799	601292	9	15
293	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	1
294	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	2
295	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	3
296	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	4
297	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	5
298	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	6
299	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	7
300	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	8
301	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	9
302	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	10
303	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	11
304	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	12
305	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	13
306	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	14
307	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	15
308	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	16
309	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	17
310	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	18

311	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	19
312	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	20
313	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	21
314	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	22
315	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	23
316	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	24
317	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	25
318	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	26
319	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	27
320	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	28
321	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	29
322	SULTX3	sulfotransferase-related protein	chr22	NM_014351	25830	0	7	30
323	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	1
324	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	2
325	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	3
326	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	4
327	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	5
328	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	6
329	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	7
330	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	8
331	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	9
332	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	10
333	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	11
334	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	12
335	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	13
336	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	14
337	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	15
338	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	16
339	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	17
340	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	18
341	TPST1	tyrosylprotein sulfotransferase 1	chr7	NM_003596	8460	603125	5	19
342	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	1
343	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	2
344	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	3
345	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	4
346	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	5
347	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	6

348	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	7
349	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	8
350	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	9
351	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	10
352	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	11
353	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	12
354	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	13
355	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	14
356	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	15
357	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	16
358	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	17
359	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	18
360	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	19
361	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	20
362	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	21
363	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	22
364	TPST2	tyrosylprotein sulfotransferase 2	chr22	NM_003595	8459	603126	7	23
365	SULT1A3	sulfotransferase family, cytosolic, 1A,	chr16	NM_003166	6818	600641	9	1
366	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	1
367	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	2
368	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	3
369	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	4
370	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	5
371	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	6
372	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	7
373	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	8
374	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	9
375	CST	galactosylceramide sulfotransferase	chr22	NM_004861	9514	602300	4	10
376	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	1
377	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	2
378	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	3
379	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	4
380	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	5
381	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	6
382	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	7
383	SULT1C1	sulfotransferase family, cytosolic, 1C, member	chr2	NM_001056	6819	602385	8	8
384	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	1

385	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	2
386	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	3
387	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	4
388	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	5
389	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	6
390	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	7
391	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	8
392	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	9
393	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	10
394	SULT1C2	SULT1C sulfotransferase	chr2	NM_006588	27233	0	7	11
395	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	1
396	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	2
397	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	3
398	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	4
399	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	5
400	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	6
401	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	7
402	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	8
403	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	9
404	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	10
405	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	11
406	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	12
407	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	13
408	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	14
409	ST1B2	thyroid hormone sulfotransferase	chr4	NM_014465	27284	0	6	15
410	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	1
411	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	2
412	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	3
413	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	4
414	CHST2	carbohydrate (chondroitin 6/keratan)	chr3	NM_004267	9435	603798	2	5
415	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	1
416	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	2
417	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	3
418	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	4
419	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	5
420	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	6
421	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	7

422	SULT2A1	sulfotransferase family, cytosolic, 2A,	chr19	NM_003167	6822	125263	6	8
423	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	1
424	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	2
425	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	3
426	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	4
427	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	5
428	SULT2B1	sulfotransferase family, cytosolic, 2B, member	chr19	NM_004605	6820	604125	6	6
429	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	1
430	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	2
431	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	3
432	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	1
433	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	2
434	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	3
435	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	4
436	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	5
437	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	6
438	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	7
439	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	8
440	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	9
441	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	10
442	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	11
443	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	12
444	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	13
445	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	14
446	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	15
447	CHST4	carbohydrate (N-acetylglucosamine 6-O)	chr16	NM_005769	10164	0	2	16
448	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	1
449	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	2
450	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	3
451	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	4
452	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	5
453	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	6
454	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	7
455	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	8
456	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	9
457	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	10
458	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	11

459	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	12
460	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	13
461	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	14
462	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	15
463	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	16
464	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	17
465	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	18
466	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	19
467	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	20
468	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	21
469	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	22
470	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	23
471	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	24
472	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	25
473	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	26
474	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	27
475	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	28
476	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	29
477	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	30
478	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	31
479	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	32
480	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	33
481	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	34
482	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	35
483	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	36
484	HNK-1ST	HNK-1 sulfotransferase	chr2	NM_004854	9486	0	6	37
485	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	1
486	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	2
487	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	3
488	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	4
489	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	5
490	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	6
491	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	7
492	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	8
493	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	9
494	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	10
495	STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	11

496 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	12
497 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	13
498 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	14
499 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	15
500 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	16
501 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	17
502 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	18
503 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	19
504 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	20
505 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	21
506 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	22
507 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	23
508 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	24
509 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	25
510 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	26
511 STE	sulfotransferase, estrogen-preferring	chr4	NM_005420	6783	600043	8	27
512 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	1
513 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	2
514 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	3
515 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	4
516 ADH1A	class I alcohol dehydrogenase, alpha subunit	chr4	NM_000667	124	103700	9	5
517 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	1
518 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	2
519 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	3
520 ADH1B	class I alcohol dehydrogenase, beta subunit	chr4	NM_000668	125	103720	9	4
521 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	1
522 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	2
523 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	3
524 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	4
525 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	5
526 ADH1C	class I alcohol dehydrogenase, gamma subunit	chr4	NM_000669	126	103730	9	6
527 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	1
528 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	2
529 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	3
530 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	4
531 ADH6	class V alcohol dehydrogenase 6	chr4	NM_000672	130	103735	8	5
532 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	1

533	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	2
534	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	3
535	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	4
536	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	5
537	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	6
538	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	7
539	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	8
540	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	9
541	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	10
542	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	11
543	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	12
544	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	13
545	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	14
546	ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	15
547	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	1
548	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	2
549	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	3
550	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	4
551	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	5
552	HEP27	short-chain alcohol dehydrogenase family member	chr14	NM_005794	10202	0	9	6
553	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	1
554	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	2
555	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	3
556	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	4
557	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	5
558	L1CAM	L1 cell adhesion molecule, isoform 1 precursor	chrX	NM_000425	3897	308840	27	6
559	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	1
560	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	2
561	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	3
562	AANAT	arylalkylamine N-acetyltransferase	chr17	NM_001088	15	600950	4	4
563	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	1
564	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	2
565	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	3
566	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	4
567	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	5
568	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	6
569	ARD1	N-acetyltransferase, homolog of S. cerevisiae	chrX	NM_003491	8260	300013	8	7

570	NAT1	N-acetyltransferase 1	chr8	NM_000662	9	108345	1	1
571	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	1
572	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	2
573	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	3
574	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	4
575	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	5
576	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	6
577	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	7
578	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	8
579	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	9
580	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	10
581	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	11
582	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	12
583	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	13
584	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	14
585	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	15
586	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	16
587	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	17
588	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	18
589	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	19
590	NAT2	arylamide acetylase 2	chr8	NM_000015	10	243400	2	20
591	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	1
592	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	2
593	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	3
594	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	4
595	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	5
596	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	6
597	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	7
598	GZMA	granzyme A precursor	chr5	NM_006144	3001	140050	5	8
599	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	1
600	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	2
601	GZMB	granzyme B precursor	chr14	NM_004131	3002	123910	5	3
602	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				1
603	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				2
604	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				3
605	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				4
606	ESD	esterase D/formylglutathione hydrolase	chr13	XM_038158				5

Fig. 235

Sulfotransferase 1C1 (*SULT1C1*)

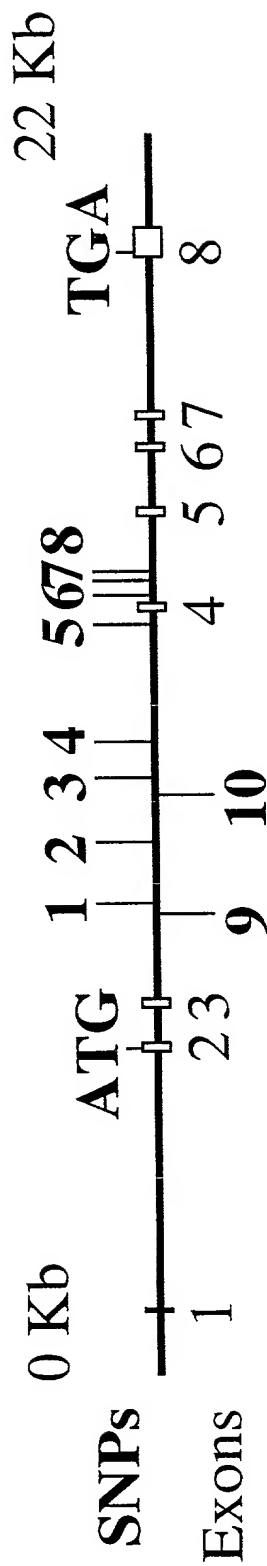
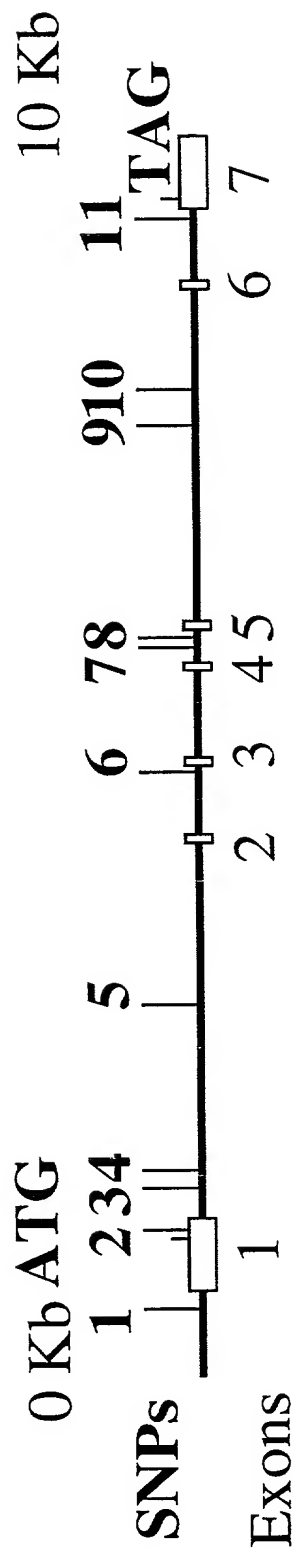


Fig. 236

Sulfotransferase 1C2 (*SULT1C2*)



680 ADH7	class IV alcohol dehydrogenase 7 mu or sigma	chr4	NM_000673	131	600086	9	16
681 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	1
682 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	2
683 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	3
684 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	4
685 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	5
686 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	6
687 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	7
688 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	8
689 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	9
690 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	10
691 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	11
692 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	12
693 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	13
694 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	14
695 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	15
696 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	16
697 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	17
698 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	18
699 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	19
700 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	20
701 GSTM1	glutathione S-transferase M1	chr4	NM_000561	2944	138350	8	21
702 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	1
703 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	2
704 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	3
705 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	4
706 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	5
707 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	6
708 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	7
709 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	8
710 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	9
711 GSTM2	glutathione S-transferase M2 (muscle)	chr1	NM_000848	2946	138380	8	10
712 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	2
713 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	3
714 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	4
715 GSTM3	glutathione S-transferase M3 (brain)	chr1	NM_000849	2947	138390	9	5
716 GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	1

717	GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	2
718	GSTM4	glutathione S-transferase M4	chr1	NM_000850	2948	138333	8	3
719	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	1
720	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	2
721	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	3
722	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	4
723	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	5
724	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	6
725	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	7
726	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	8
727	GSTZ1	glutathione transferase zeta 1	chr14	NM_001513	2954	603758	9	9
728	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	1
729	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	2
730	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	3
731	GSTP1	glutathione transferase	chr11	NM_000852	2950	134660	7	4
732	GSTT1	glutathione S-transferase theta 1	chr22	NM_000853	2952	600436	5	1
733	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	1
734	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	2
735	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	3
736	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	4
737	PTGES	prostaglandin E synthase	chr18	NM_004878	9536	605172	4	5
738	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	1
739	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	2
740	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	3
741	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	4
742	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	5
743	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	6
744	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	7
745	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	8
746	MGST2	microsomal glutathione S-transferase 2	chr4	NM_002413	4258	601733	5	9
747	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	1
748	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	2
749	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	3
750	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	4
751	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	5
752	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	6
753	MGST3	microsomal glutathione S-transferase 3	chr1	NM_004528	4259	604564	5	7

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male			
Marital status	Married			
Education	High school			
Occupation	Teacher			
Income	Low			
Health status	Good			
Stress level	High			
Life satisfaction	Low			
Resilience	Low			
Optimism	Low			
Self-efficacy	Low			
Emotional stability	Low			
Neuroticism	High			
Extraversion	Low			
Conscientiousness	Low			
Agreeableness	Low			
Openness	Low			
Depression	High			
Anxiety	High			
Post-traumatic stress disorder	High			
Substance use	Low			
Alcohol consumption	Low			
Drug use	Low			
Smoking	Low			
Exercise	Low			
Diet	Low			
Sleep	Low			
Work-life balance	Low			
Family support	Low			
Community support	Low			
Religious/spiritual beliefs	Low			
Philosophical beliefs	Low			
Political beliefs	Low			
Cultural beliefs	Low			
Personal beliefs	Low			
Values	Low			
Attitudes	Low			
Beliefs	Low			
Opinions	Low			
Preferences	Low			
Interests	Low			
Hobbies	Low			
Skills	Low			
Talents	Low			
Strengths	Low			
Weaknesses	Low			
Assets	Low			
Liabilities	Low			
Resources	Low			
Capabilities	Low			
Potential	Low			
Opportunities	Low			
Challenges	Low			
Risks	Low			
Uncertainties	Low			
Unknowns	Low			
Variables	Low			
Factors	Low			
Elements	Low			
Components	Low			
Parts	Low			
Sections	Low			
Divisions	Low			
Subdivisions	Low			
Categories	Low			
Classes	Low			
Groups	Low			
Clusters	Low			
Networks	Low			
Systems	Low			
Structures	Low			
Frameworks	Low			
Models	Low			
Theories	Low			
Hypotheses	Low			
Propositions	Low			
Assertions	Low			
Statements	Low			
Declarations	Low			
Announcements	Low			
Revelations	Low			
Disclosures	Low			
Exposures	Low			
Uncoverings	Low			
Unfoldings	Low			
Unrollings	Low			
Unwrappings	Low			
Unpeelings	Low			
Uncoverings	Low			
Unfoldings	Low			
Unrollings	Low			
Unwrappings	Low			
Unpeelings	Low			
Uncoverings	Low			
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Uncoverings	Low			
Unfoldings	Low			
Unrollings	Low			
Unwrappings	Low			
Unpeelings	Low			
Uncoverings	Low			
Unfoldings	Low			
Unrollings	Low			
Unwrappings	Low			

Observed	:	T/C
3' Assay	:	ACAAGCCATT GCGCTAGAGA GAGCCATCTG CAGTTCTCC TTAGACAGAT GTTCAGATGG
Comment	:	
Sample size	:	96

Screened Sequence

Accession No.	:	NT_024413.3 (Graphical View of this Entry)
Chromosome	:	12
map	:	
Definition of the record	:	Homo sapiens chromosome 12 working draft sequence segment.
Position in sequence	:	536287 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID	:	NT_024413.3_20010417_1	
Amplified region	:	536137..536950 in NT_024413	
size	:	814	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTGAGAACAT GAGCGTGTGT	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892

12/17/2001

791	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha	chrX	NM_004541	4694	300078	3	5
792	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	1
793	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	2
794	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	3
795	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	4
796	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	5
797	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	6
798	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha	chr5	NM_002488	4695	602137	3	6
799	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_004542	4696	603832	4	1
800	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_004542	4696	603832	4	2
801	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_004542	4696	603832	4	3
802	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	1
803	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	2
804	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	3
805	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	4
806	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	5
807	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	5
808	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	6
809	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha	chr7	NM_005000	4698	601677	5	7
810	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	1
811	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	2
812	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	3
813	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	4
814	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	5
815	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	6
816	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha	chr22	NM_002490	4700	602138	3	6
817	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	1
818	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	2
819	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	3
820	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	4
821	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	5
822	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	6
823	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	7
824	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	8
825	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	9
826	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	10
827	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	11

828	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	12
829	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	12
830	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	13
831	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha	chr19	NM_005001	4701	602139	4	14
832	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	1
833	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	2
834	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	3
835	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	4
836	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	5
837	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	6
838	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	7
839	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	8
840	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	9
841	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	10
842	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	11
843	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	12
844	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	12
845	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	13
846	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha	chr9	NM_014222	4702	603359	4	13
847	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta	chr16	NM_005003	4706	603836	5	1
848	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta	chr16	NM_005003	4706	603836	5	2
849	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	1
850	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	2
851	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	3
852	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	4
853	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	5
854	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	6
855	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	7
856	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	8
857	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	9
858	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	10
859	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	11
860	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	12
861	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	13
862	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	14
863	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	15
864	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	16

865	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	17
866	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	18
867	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	19
868	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	20
869	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	21
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871	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	23
872	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	24
873	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	25
874	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	26
875	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	27
876	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	28
877	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	29
878	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	30
879	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	31
880	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	32
881	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	33
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885	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	37
886	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	38
887	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	39
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889	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	40
890	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha	chr12	NM_005002	4704	603834	11	41
891	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	1
892	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	2
893	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	3
894	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	4
895	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	5
896	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	6
897	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	7
898	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	8
899	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	9
900	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	10
901	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	chr2	NM_005006	4719	157655	19	11

SNP Information for IMS-JST104848

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST104848
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_028388.2	301178	19	71733798

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011148.3	genomic	NDUFA3	CDS*1	Annotated	

939	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	6
940	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	7
941	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	8
942	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	9
943	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	10
944	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	11
945	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	12
946	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	13
947	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	14
948	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	15
949	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	16
950	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	17
951	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	18
952	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	19
953	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	20
954	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	21
956	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	22
957	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	chr1	NM_004552	4725	603847	2	24
958	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	1
959	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	2
960	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	3
961	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	4
962	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	5
963	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	6
964	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	7
965	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	8
966	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	9
967	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	10
968	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	11
969	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	12
970	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	13
971	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	14
972	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	15
973	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	16
974	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	17
975	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	18
976	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	chr5	NM_004553	4726	603848	4	19

PCR Condition

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : GTAGATGGAA GATAGTAGGC A
BackwardPrimer : AGGATCAGTT CCATTCTGC AC



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104949

12/17/2001

[illegible]

1199	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	7
1200	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	8
1201	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	9
1202	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	10
1203	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	11
1204	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	12
1205	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	12
1206	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	13
1207	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	14
1207	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	14
1209	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	15
1210	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	16
1211	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	16
1212	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	17
1213	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	18
1214	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	19
1215	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	20
1216	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	21
1217	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	22
1218	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	23
1219	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	24
1220	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	25
1221	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	26
1222	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	27
1223	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	28
1224	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	29
1225	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	30
1226	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	31
1227	HNMT	histamine N-methyltransferase	chr2	NM_006895	3176	605238	6	32
1228	GAMT	guanidinoacetate N-methyltransferase	chr19	NM_000156	2593	601240	6	3
1229	PNMT	phenylethanolamine N-methyltransferase	chr17	NM_002686	5409	171190	3	2
1230	CYP1A1	cytochrome P450, subfamily I (aromatic	chr15	NM_000499	1543	108330	7	1
1231	CYP1A1	cytochrome P450, subfamily I (aromatic	chr15	NM_000499	1543	108330	7	2
1232	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	1
1233	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	2
1234	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	3
1235	CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	4

1236 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	5
1237 CYP1A2	cytochrome P450, subfamily I (aromatic	chr15	NM_000761	1544	124060	7	6
1238 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	1
1239 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	2
1240 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	3
1241 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	4
1242 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	5
1243 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	6
1244 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	7
1245 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	8
1246 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	8
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1249 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	11
1250 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	11
1251 CYP1B1	cytochrome P450, subfamily I (dioxin-inducible),	chr2	NM_000104	1545	601771	3	12
1252 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	90
1253 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	91
1254 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	92
1255 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	93
1256 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	94
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1258 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	96
1259 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	97
1260 PENT	phosphatidylethanolamine N-methyltransferase	chr17	NM_007169	10400	602391	7	98
1261 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	21
1262 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	22
1263 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	23
1264 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	24
1265 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	25
1266 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	26
1267 NAT2	arylamine acetylase 2	chr8	NM_000015	10	243400	2	27
1268 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	1
1269 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	2
1270 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	3
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1272 AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	5

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1278	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	11
1279	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	12
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1287	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	20
1288	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	21
1289	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	22
1290	NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	1
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1296	NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	7
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1304	NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	15
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1307	NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	18
1308	NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	19
1309	NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	20

1310 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	21
1311 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	22
1312 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	23
1313 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	24
1314 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	25
1315 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	26
1316 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	27
1317 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	28
1318 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	29
1319 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	30
1320 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	31
1321 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	32
1322 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	33
1323 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	34
1324 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	35
1325 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	36
1326 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	37
1327 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	38
1328 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	39
1329 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	40
1330 NTE	neuropathy target esterase	chr19	NM_006702	10908	603197	35	41
1331 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	8
1332 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	9
1333 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	10
1334 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	11
1335 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	12
1336 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	13
1337 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	14
1338 DDOST	dolichyl-diphosphooligosaccharide-protein	chr1	NM_005216	1650	602202	11	15
1339 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	1
1340 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	2
1341 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	3
1342 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	4
1343 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	5
1344 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	6
1345 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	7
1346 ABCC2	ATP-binding cassette, sub-family C (CFTR/MRP),	chr10	NM_000392	1244	601107	32	8

[illegible]

1384 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	4
1385 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	5
1386 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	6
1387 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	7
1388 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	8
1389 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	9
1390 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	10
1391 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	11
1392 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	12
1393 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	13
1394 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	14
1395 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	15
1396 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	16
1397 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	17
1398 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	18
1399 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	19
1400 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	20
1401 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	21
1402 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	22
1403 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	23
1404 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	24
1405 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	25
1406 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	26
1407 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	27
1408 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	28
1409 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	29
1410 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	30
1411 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	31
1412 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	32
1413 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	33
1414 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	34
1415 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	35
1416 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	36
1417 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	37
1418 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	37
1419 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	38
1421 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	1

1422 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	2
1423 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	3
1424 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	4
1425 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	5
1426 TAP1	transporter 1, ATP-binding cassette, sub-family	chr6	NM_000593	6890	170260	11	6
1427 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	1
1428 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	2
1429 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	3
1430 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	4
1431 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	5
1432 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	6
1433 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	7
1434 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	8
1435 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	9
1436 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	10
1437 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	10
1438 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	11
1439 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	12
1440 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	13
1441 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	14
1442 ABCB7	ATP-binding cassette, sub-family B, member 7	chrX	NM_004299	22	300135	14	15
1443 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	1
1444 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	2
1445 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	3
1446 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	4
1447 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	5
1448 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	6
1449 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	7
1450 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	8
1451 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	9
1452 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	10
1453 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	11
1454 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	12
1455 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	13
1456 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	14
1457 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	14
1458 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	15

1459 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	16
1460 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	17
1461 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	18
1462 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	19
1463 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	20
1464 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	21
1465 ABCB8	ATP-binding cassette, sub-family B, member 8	chr7	NM_007188	11194	605464	16	22
1466 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	1
1467 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	2
1468 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	3
1469 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	4
1470 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	5
1471 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	6
1472 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	7
1473 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	8
1474 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	9
1475 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	10
1476 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	11
1477 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	12
1478 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	13
1479 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	14
1480 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	15
1481 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	16
1482 ABCB9	ATP-binding cassette, sub-family B, member 9,	chr12	NM_019624	23457	605453	11	17
1483 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	1
1484 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	2
1485 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	3
1486 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	4
1487 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	5
1488 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	6
1489 ABCB1	ATP-binding cassette, sub-family B (MDR/TAP),	chr7	NM_000927	5243	171050	29	7
1490 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	8
1491 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	9
1492 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	10
1493 ABCB10	ATP-binding cassette, sub-family B, member 10	chr1	NM_012089	23456	605454	13	11
1494 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	1
1495 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	28	1

[illegible]

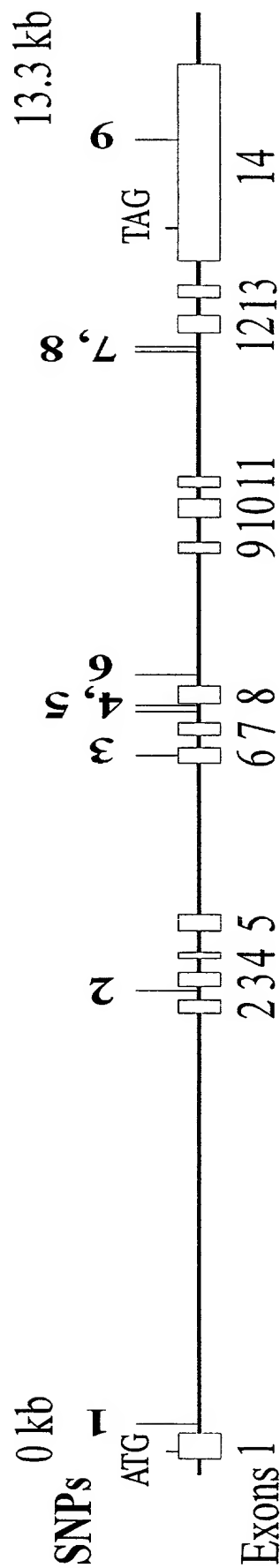
[illegible]

1571 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	71
1572 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	72
1573 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	72
1574 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	73
1575 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	74
1576 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	75
1577 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	76
1578 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	77
1579 ABCB11	ATP-binding cassette, sub-family B (MDR/TAP),	chr2	NM_003742	8647	603201	78
1580 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	1
1581 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	2
1582 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	3
1583 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	4
1584 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	5
1585 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	6
1586 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	7
1587 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	8
1588 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	9
1589 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	10
1590 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	11
1591 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12
1592 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	13
1593 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	14
1594 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	15
1595 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	16
1596 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	17
1597 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	18
1598 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	19
1600 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	20
1601 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	21
1602 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	22
1603 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	23
1604 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	24
1605 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	25
1606 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	26
1607 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	27
1608 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	28

1609 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	29
1610 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	30
1611 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	31
1612 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	32
1613 CYP4B1	cytochrome P450, subfamily IVB, polypeptide 1	chr1	NM_000779	1580	124075	12	33
1614 CYP27A1	cytochrome P450, subfamily XXVIIA, polypeptide 1	chr2	NM_000784	1593	213700	9	1
1615 CYP27A1	cytochrome P450, subfamily XXVIIA, polypeptide 1	chr2	NM_000784	1593	213700	9	2
1616 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	1
1617 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	2
1618 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	3
1619 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	4
1620 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	5
1621 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	6
1622 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	7
1623 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	8
1624 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	9
1625 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	10
1626 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	11
1627 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	12
1628 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	13
1629 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	14
1630 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	15
1631 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	16
1632 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	17
1633 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	18
1634 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	19
1635 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	20
1636 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	21
1637 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	22
1638 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	23
1639 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	23
1640 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	24
1641 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	25
1642 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	26
1643 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	27
1644 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	28
1645 CYP4F2	cytochrome P450, subfamily IVF, polypeptide 2	chr19	NM_001082	8529	604426	13	29

Fig. 168

ATP binding cassette, subfamily G, member 4 (*ABCG4*)



1683 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	4
1684 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	5
1685 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	6
1686 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	7
1687 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	8
1688 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	9
1689 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	10
1690 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	11
1691 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	11
1692 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	12
1693 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	13
1694 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	14
1695 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	15
1696 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	16
1697 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	17
1698 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	18
1699 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	19
1700 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	20
1701 CYP4F8	cytochrome P450, subfamily IVF, polypeptide 8	chr19	NM_007253	11283	0	12	21
1702 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	1
1703 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	2
1704 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	3
1705 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	4
1706 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	5
1707 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	6
1708 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	7
1709 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	8
1710 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	9
1711 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	10
1712 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	11
1713 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	12
1714 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	13
1715 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	14
1716 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	15
1717 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	16
1718 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	17
1719 ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	17

1720	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	18
1721	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	19
1722	ALDH1	aldehyde dehydrogenase 1, soluble	chr9	NM_000689	216	100640	13	20
1723	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	1
1724	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	2
1725	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	3
1726	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	4
1727	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	5
1728	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	6
1729	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	7
1730	ALDH2	aldehyde dehydrogenase 2, mitochondrial	chr12	NM_000690	217	100650	13	8
1731	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	1
1732	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	2
1733	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	3
1734	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	4
1735	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	5
1736	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	6
1737	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	7
1738	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	8
1739	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	9
1740	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	10
1741	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	11
1742	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	12
1743	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	13
1744	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	14
1745	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	15
1746	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	16
1747	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	17
1748	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	18
1749	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	19
1750	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	20
1751	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	21
1752	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	22
1753	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	23
1754	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	24
1755	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	25
1756	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	26

1757	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	27
1758	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	28
1759	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	29
1760	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	30
1761	ALDH3B1	aldehyde dehydrogenase 3B1	chr11	NM_000694	221	600466	11	31
1762	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	1
1763	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	2
1764	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	3
1765	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	4
1766	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	5
1767	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	6
1768	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	7
1769	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	8
1770	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	9
1771	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	10
1772	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	10
1773	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	11
1774	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	12
1775	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	13
1776	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	14
1777	ALDH3B2	aldehyde dehydrogenase 3B2	chr11	NM_000695	222	601917	10	15
1778	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	1
1779	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	2
1780	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	3
1781	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	4
1782	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	5
1783	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	6
1784	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	7
1785	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	8
1786	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	9
1787	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	10
1788	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	11
1789	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	12
1790	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	13
1791	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	14
1792	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	15
1793	ALDH9	aldehyde dehydrogenase 9	chr1	NM_000696	223	602733	11	16

Fig. 209 Alcohol dehydrogenase 1 (*ADH1*)

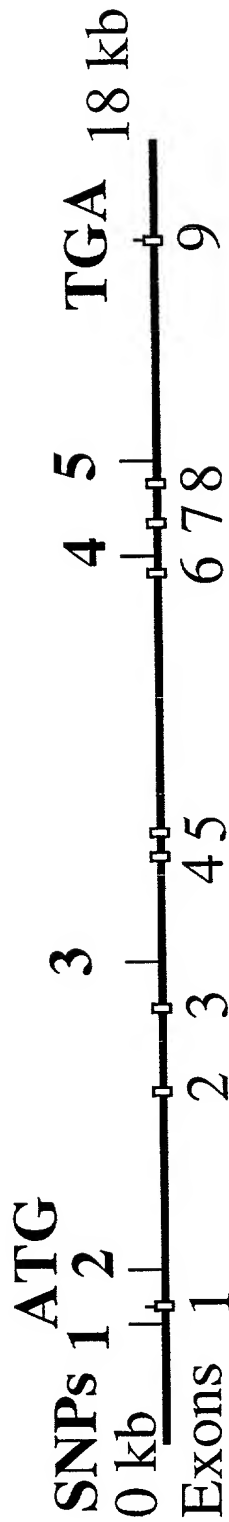


Fig. 210 Alcohol dehydrogenase 2 (*ADH2*)

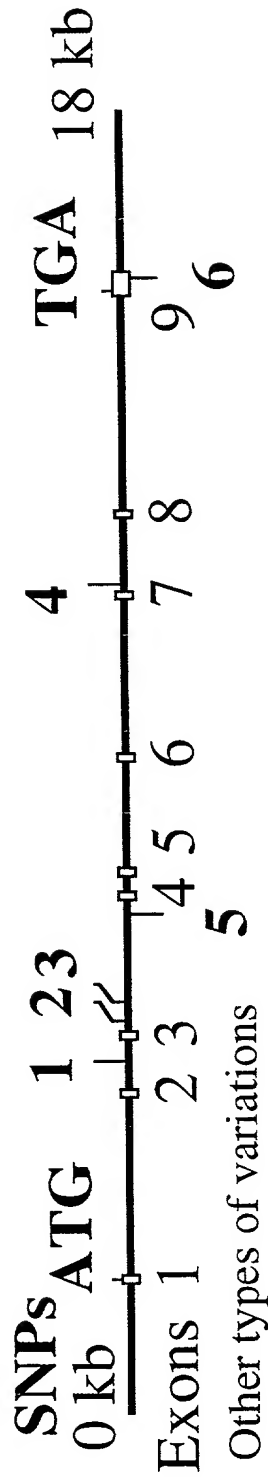
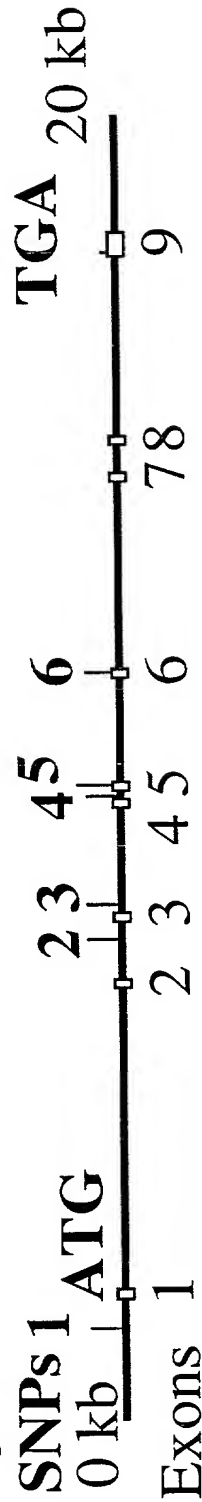


Fig. 211 Alcohol dehydrogenase 3 (*ADH3*)



1869 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	45
1870 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	46
1871 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	47
1872 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	48
1873 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	49
1874 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	50
1875 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	51
1876 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	52
1877 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	53
1878 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	54
1879 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	55
1880 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	56
1881 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	57
1882 CFTR	cystic fibrosis transmembrane conductance	chr7	NM_000492	1080	602421	27	58
1883 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	1
1884 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	2
1885 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	3
1886 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	4
1887 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	5
1888 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	6
1889 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	7
1890 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	8
1891 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	9
1892 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	9
1893 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	10
1894 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	11
1895 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	12
1896 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	13
1897 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	14
1898 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	15
1899 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	16
1900 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	17
1901 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	18
1902 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	19
1903 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	20
1904 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	21
1905 ABCC8	ATP-binding cassette, sub-family C, member 8	chr11	NM_000352	6833	600509	39	22

[illegible]

[illegible]

TABLE "EESSEOT"

2017 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	44
2018 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	45
2019 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	46
2020 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	47
2021 ABCC9	ATP-binding cassette, sub-family C, member 9,	chr12	NM_005691	10060	601439	38	48
2022 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	1
2023 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	2
2024 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	3
2025 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	4
2026 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	5
2027 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	6
2028 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	7
2029 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	8
2030 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	9
2031 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	10
2032 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	11
2033 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	12
2034 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	13
2035 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	14
2036 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	15
2037 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	16
2038 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	17
2039 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	18
2040 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	19
2041 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	20
2042 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	21
2043 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	21
2044 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	22
2045 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	23
2046 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	24
2047 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	25
2048 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	26
2049 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	27
2050 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	28
2051 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	29
2052 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	30
2053 CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	31

2054	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	32
2055	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	33
2056	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	34
2057	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	35
2058	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	36
2059	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	37
2060	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	38
2061	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	39
2062	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	40
2063	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	41
2064	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	42
2065	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	43
2066	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	44
2067	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	45
2068	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	46
2069	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	47
2070	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	48
2071	CES1	carboxylesterase 1 (monocyte/macrophage serine	chr16	NM_001266	1066	114835	14	49
2072	ABCB4	ATP-binding cassette, subfamily B, member 4,	chr7	NM_000443	5244	171060	32	33
2073	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	23
2074	AADAC	arylacetamide deacetylase	chr3	NM_001086	13	600338	6	24
2075	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	1
2076	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	2
2077	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	3
2078	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	4
2079	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	5
2080	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	6
2081	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	7
2082	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	8
2083	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	9
2084	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	10
2085	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	11
2086	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	12
2087	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	13
2088	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	14
2089	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	15
2090	ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	16

[illegible][illegible]

2277 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	199
2278 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	200
2279 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	201
2280 ABCA4	ATP-binding cassette, sub-family A member 4	chr1	NM_000350	24	601691	50	202
2281 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	1
2282 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	2
2283 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	3
2284 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	4
2285 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	5
2286 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	6
2287 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	7
2288 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	8
2289 BCCA7							9
2290 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	10
2291 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	11
2292 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	12
2293 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	13
2294 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	14
2295 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	15
2296 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	16
2297 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	17
2298 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	18
2299 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	19
2300 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	20
2301 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	21
2302 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	22
2303 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	23
2304 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	24
2305 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	25
2306 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	26
2307 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	27
2308 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	28
2309 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	29
2310 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	30
2311 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	31
2312 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	32
2313 ABCA7	ATP-binding cassette, sub-family A member 7,	chr19	NM_019112	10347	605414	46	33

2351 ABCA7	ATP-binding cassette, sub-family A, member 7,	chr19	NM_019112	10347	605414	46	71
2352 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	1
2353 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	2
2354 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	3
2355 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	4
2356 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	5
2357 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	6
2358 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	7
2359 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	8
2360 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	9
2361 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	10
2362 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	11
2363 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	12
2364 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	13
2365 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	14
2366 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	15
2367 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	16
2368 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	17
2369 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	18
2370 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	19
2371 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	20
2372 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	21
2373 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	22
2374 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	23
2375 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	24
2376 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	25
2377 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	26
2378 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	27
2379 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	28
2380 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	29
2381 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	30
2382 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	31
2383 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	32
2384 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	33
2385 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	34
2386 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	35
2387 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	36

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2425 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	74
2426 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	75
2427 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	76
2428 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	77
2429 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	78
2430 ABCG1	ATP-binding cassette sub-family G member 1	chr21	NM_004915	9619	603076	15	79
2431 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	1
2432 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	2
2433 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	3
2434 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	4
2435 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	5
2436 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	6
2437 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	7
2438 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	8
2439 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	9
2440 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	10
2441 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	11
2442 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	12
2443 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	13
2444 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	14
2445 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	15
2446 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	16
2447 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	17
2448 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	18
2449 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	19
2450 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	20
2451 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	21
2452 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	22
2453 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	23
2454 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	24
2455 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	25
2456 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	26
2457 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	27
2458 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	28
2459 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	29
2460 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	30
2461 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	31

2462 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	32
2463 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	33
2464 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	34
2465 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	35
2466 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	36
2467 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	37
2468 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	38
2469 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	39
2470 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	40
2471 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	41
2472 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	42
2473 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	43
2474 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	44
2475 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	45
2476 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	46
2477 ABCG2	ATP-binding cassette, sub-family G, member 2	chr4	NM_004827	9429	603756	16	47
2478 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	1
2479 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	2
2480 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	3
2481 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	4
2482 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	5
2483 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	6
2484 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	7
2485 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	8
2486 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	9
2487 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	10
2488 ABCG4	ATP-binding cassette, subfamily G, member 4	chr11	NM_022169	64137	0	13	11
2489 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	1
2490 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	2
2491 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	3
2492 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	4
2493 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	5
2494 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	6
2495 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	7
2496 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	8
2497 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	9
2498 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	10

2499 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	11
2500 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	11
2501 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	12
2502 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	13
2503 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	14
2504 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	15
2505 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	16
2506 ABCE1	ATP-binding cassette, sub-family E, member 1	chr4	NM_002940	6059	601213	18	17
2507 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	1
2508 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	2
2509 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	3
2510 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	4
2511 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	5
2512 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	6
2513 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	7
2514 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	8
2515 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	9
2516 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	10
2517 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	11
2518 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	12
2519 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	13
2520 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	14
2521 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	15
2522 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	16
2523 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	17
2524 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	18
2525 CHST1	carbohydrate (chondroitin 6/keratan)	chr11	NM_003654	8534	603797	4	19
2526 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	1
2527 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	2
2528 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	3
2529 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	4
2530 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	5
2531 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	6
2532 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	7
2533 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	8
2534 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	9
2535 CHST3	carbohydrate (chondroitin 6/keratan)	chr10	NM_004273	9469	603799	7	10

Sequence

Observed : A/G
 3' Assay : CCGTGGTTCA TGCCGTGTAAT CCGAGCACTA TGGGAGGCCG AGACGGCGG ATCACCAGGT
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011190.3 (Graphical View of this Entry)
 Chromosome : 19
 map
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
 Position in Sequence : 1120657 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011190.3.20010417_4
 Amplified region : 1120220..1121152 in NT_011190
 size : 933

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGTGAATAAC TATGTACCA	G

2610	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	3
2611	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	4
2612	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	5
2613	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	6
2614	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	7
2615	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	8
2616	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	9
2617	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	10
2618	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3	chr21	NM_021075	4731	602184	3	11
2619	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	1
2620	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	2
2621	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	3
2622	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	4
2623	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	5
2624	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	6
2625	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	7
2626	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	8
2627	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	9
2628	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	10
2629	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	11
2630	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	12
2631	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	13
2632	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	14
2633	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	15
2634	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	16
2635	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	17
2636	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	18
2637	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	19
2638	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	20
2639	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	21
2640	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	22
2641	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	23
2642	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	24
2643	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	25
2644	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	26
2645	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	27
2646	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	28

2647	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	29
2648	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	30
2649	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	31
2650	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	32
2651	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	33
2652	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	34
2653	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	35
2654	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	36
2655	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	37
2656	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	37
2657	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	38
2658	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	39
2659	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	40
2660	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	40
2661	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	41
2662	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha	chr2	NM_004544	4705	603835	10	42
2663	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	37
2664	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	38
2665	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	39
2666	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	40
2667	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	41
2668	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	42
2669	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	43
2670	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	44
2671	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	45
2672	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	46
2673	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	47
2674	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	48
2675	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	49
2676	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	50
2677	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	51
2678	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	52
2680	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	54
2681	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	55
2682	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	56
2683	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	57
2684	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	58

2685	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	59
2686	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	60
2687	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	61
2688	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	62
2689	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	63
2690	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	64
2691	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	65
2692	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	66
2693	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	67
2694	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	68
2695	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	69
2696	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	70
2697	MGST1	microsomal glutathione S-transferase 1	chr12	NM_020300	4257	138330	4	71
2698	HMG17L1	high-mobility group (nonhistone chromosomal)	chr22	NM_021024	23605	0	2	1
2699	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	1
2700	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	2
2701	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	3
2702	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	4
2703	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	5
2704	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	6
2705	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	7
2706	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	8
2707	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	9
2708	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	10
2709	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	11
2710	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	12
2711	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	13
2712	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	14
2713	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	15
2714	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	16
2715	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	17
2716	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	18
2717	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	19
2718	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	20
2719	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	21
2720	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	22
2721	UGT2A1	UDP glycosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	23

2759	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	61
2760	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	62
2761	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	63
2762	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	64
2763	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	65
2764	UGT2A1	UDP glucosyltransferase 2 family, polypeptide	chr4	NM_006798	10941	604716	6	66
2765	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	1
2766	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	2
2767	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	3
2768	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	4
2769	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	5
2770	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	6
2771	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	7
2772	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	8
2773	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	9
2774	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	10
2775	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	11
2776	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	12
2777	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	13
2778	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	14
2779	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	15
2780	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	16
2781	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	17
2782	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	18
2783	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	19
2784	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	20
2785	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	21
2786	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	22
2787	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	23
2788	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	24
2789	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	25
2790	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	26
2791	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	27
2792	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	28
2793	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	29
2794	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	30
2795	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	31

2796	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	32
2797	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	33
2798	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	34
2799	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	35
2800	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	36
2801	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	37
2802	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	38
2803	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	39
2804	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	40
2805	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	41
2806	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	42
2807	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	43
2808	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	44
2809	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	45
2810	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	46
2811	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	47
2812	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	48
2813	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	49
2814	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	50
2815	SLC21A3	solute carrier family 21 member 3	chr12	NM_005075	6579	602883	13	51
2816	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	1
2817	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	2
2818	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	3
2819	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	4
2820	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	5
2821	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	6
2822	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	7
2823	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	8
2824	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	9
2825	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	10
2826	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	11
2828	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	12
2829	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	14
2830	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	15
2831	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	16
2832	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	17
2833	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	18

PCR "EE3E00"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCCTCAGGTA CTCCTACCTA G
BackwardPrimer : CGTGCCTTCTA CCTTCTATTA C



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104980

2908	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	93
2909	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	94
2910	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	95
2911	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	96
2912	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	97
2913	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	98
2914	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	99
2915	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	100
2916	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	101
2917	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	102
2918	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	103
2919	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	104
2920	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	105
2921	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	106
2922	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	107
2923	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	108
2924	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	109
2925	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	110
2926	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	111
2927	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	112
2928	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	113
2929	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	114
2930	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	115
2931	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	116
2932	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	117
2933	SLC21A6	solute carrier family 21 member 6	chr12	NM_006446	10599	604843	15	118
2934	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	1
2935	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	2
2936	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	3
2937	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	4
2938	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	5
2939	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	6
2940	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	7
2941	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	8
2942	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	9
2943	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	10
2944	SLC21A8	solute carrier family 21 (organic anion)	chr12	NM_019844	28234	605495	14	11

[illegible]

[illegible]

3020	SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	6
3021	NAT1	N-acetyltransferase 1	chr8	NM_000662	9	108345	1	7
3022	SLC22A6	solute carrier family 22 (organic anion	chr11	NM_004790	9356	0	10	8
3023	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	1
3024	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	2
3025	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	3
3026	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	4
3027	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	5
3028	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	6
3029	SLC22A7	solute carrier family 22 (organic anion	chr6	NM_006672	10864	604995	10	7
3030	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	1
3031	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	2
3032	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	3
3033	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	4
3034	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	5
3035	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	6
3036	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	7
3037	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	8
3038	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	9
3039	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	10
3040	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	11
3041	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	12
3042	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	13
3043	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	14
3044	SLC22A8	solute carrier family 22 (organic anion	chr11	NM_004254	9376	0	9	15
3045	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	1
3046	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	2
3047	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	3
3048	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	4
3049	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	5
3050	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	6
3051	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	7
3052	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	8
3053	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	9
3054	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	10
3055	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	11
3056	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888			13	12

SNP Information



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Keyword

search

SNP Information for IMS-JST105327

General Information

JSNP ID : IMS-JST105327
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1324484	9	98923950

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

3131	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	85
3132	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	86
3133	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	87
3134	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	88
3135	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	89
3136	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	90
3137	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	91
3138	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	92
3139	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	93
3140	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	94
3141	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	95
3142	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	96
3143	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	97
3144	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	98
3145	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	99
3146	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	100
3147	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	101
3148	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	102
3149	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	103
3150	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	104
3151	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	105
3152	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	106
3153	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	107
3154	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	108
3155	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	108
3156	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	109
3157	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	109
3158	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	110
3159	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	111
3160	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	112
3161	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	113
3162	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	114
3163	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	115
3164	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	116
3165	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	chr15	NM_003888	13	117
3166	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463
3167	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463

TABLE 1

3168	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	3
3169	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	4
3170	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	4
3171	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	5
3172	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	6
3173	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	7
3174	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	8
3175	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	9
3176	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	10
3177	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	11
3178	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	12
3179	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	13
3180	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	14
3181	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	15
3182	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	16
3183	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	17
3184	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	18
3185	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	19
3186	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	20
3187	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	21
3188	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	22
3189	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	23
3190	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	24
3191	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	25
3192	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	26
3193	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	27
3194	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	28
3195	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	29
3196	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	30
3198	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	31
3199	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	32
3200	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	33
3201	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	34
3202	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	35
3203	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	36
3204	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	37
3205	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	38

3206	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	39
3207	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	40
3208	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	41
3209	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	42
3210	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	43
3211	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	44
3212	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	45
3213	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	46
3214	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	47
3215	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	48
3216	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	49
3217	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	50
3218	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	51
3219	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	52
3220	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	53
3221	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	54
3222	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	55
3223	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	56
3224	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	57
3225	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	58
3226	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	59
3227	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	60
3228	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	61
3229	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	62
3230	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	63
3231	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	64
3232	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	65
3233	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	66
3234	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	67
3235	ALDH1A3	aldehyde dehydrogenase 1A3	chr15	NM_000693	220	600463	13	68
3236	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	1
3237	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	2
3238	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	3
3239	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	4
3240	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	5
3241	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	6
3242	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	7

3316	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	78
3317	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	79
3318	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	80
3319	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	81
3320	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	82
3321	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	83
3322	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	84
3323	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	85
3324	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	86
3325	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	87
3326	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	88
3327	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	89
3328	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	90
3329	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	91
3330	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	92
3331	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	93
3332	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	94
3333	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	95
3334	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	96
3335	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	97
3336	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	98
3337	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	99
3338	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	100
3339	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	101
3340	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	102
3341	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	103
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3343	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	105
3344	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	106
3345	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	107
3346	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	108
3347	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	109
3348	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	110
3349	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	111
3350	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	112
3351	FTHFD	formyltetrahydrofolate dehydrogenase	chr3	NM_012190	10840	600249	13	113
3352	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	1

Table 1: Gene list

3353	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	2
3354	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	3
3355	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	4
3356	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	4
3357	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	5
3358	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	6
3359	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	7
3360	CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4	chr7	NM_017460	1576	124010	13	8

Fig. 144A ATP binding cassette, subfamily A, member 1
(ABCA1)

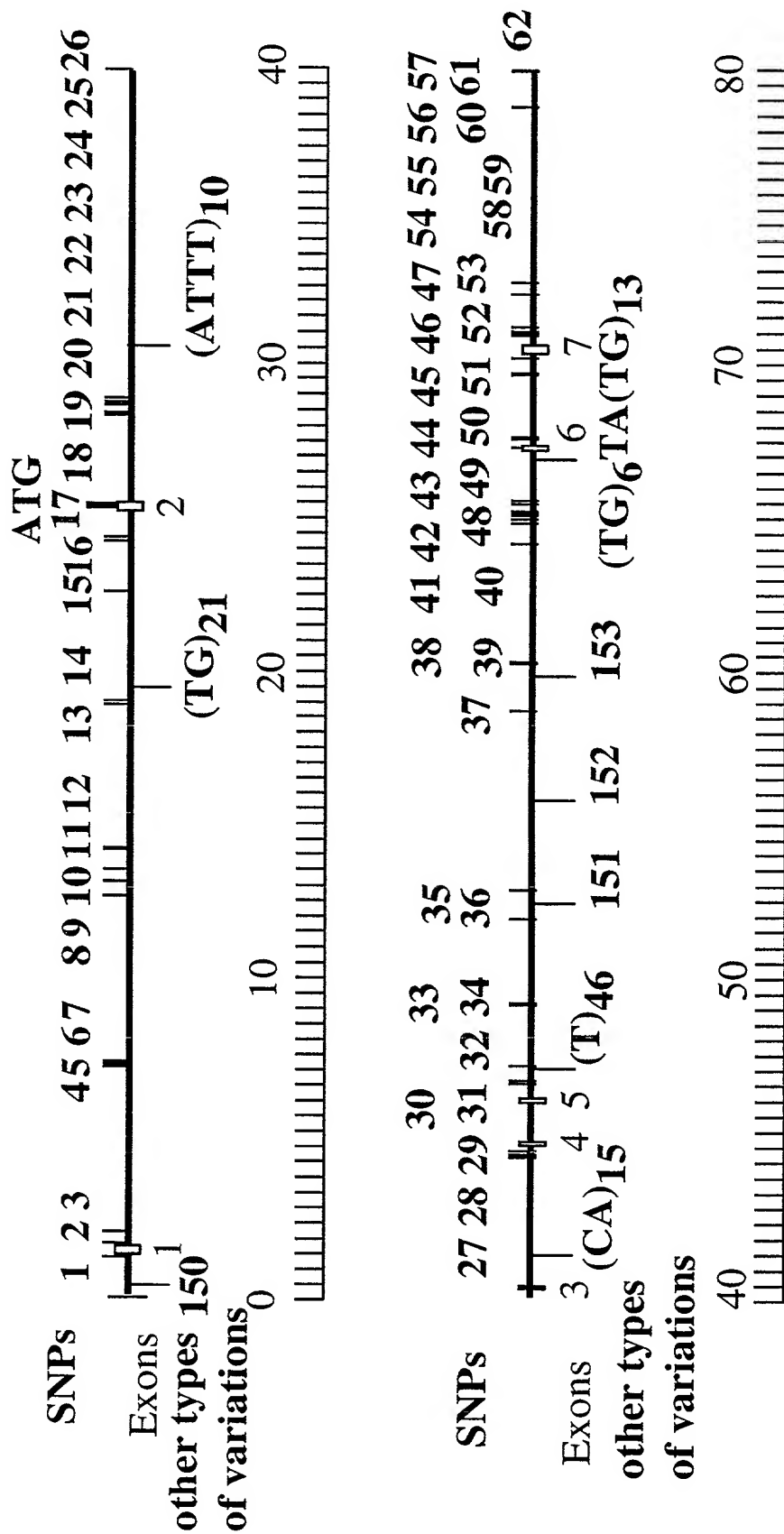


Fig. 144 B

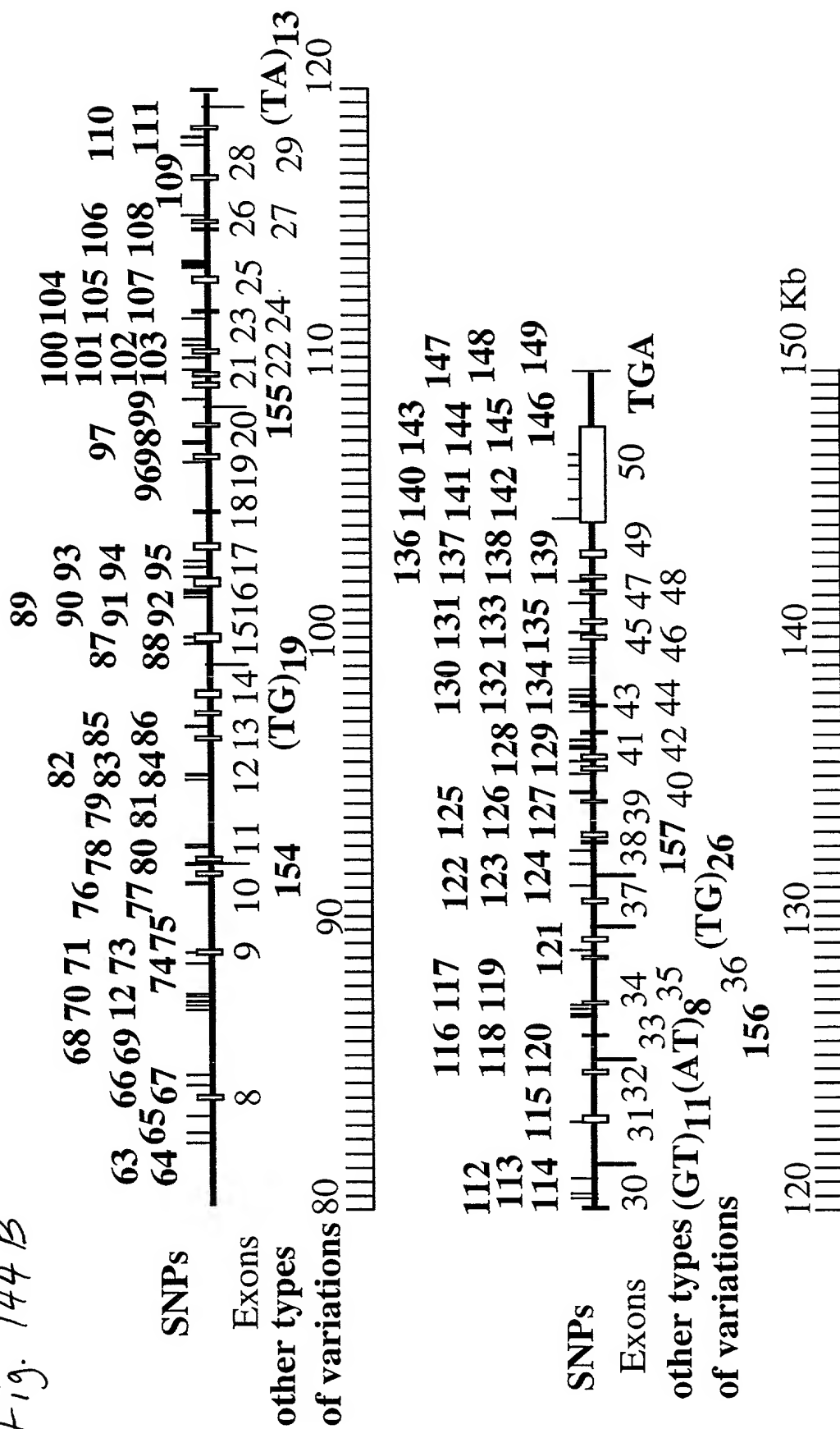


Fig. 145 ATP binding cassette, subfamily A, member 4 (ABCA4)

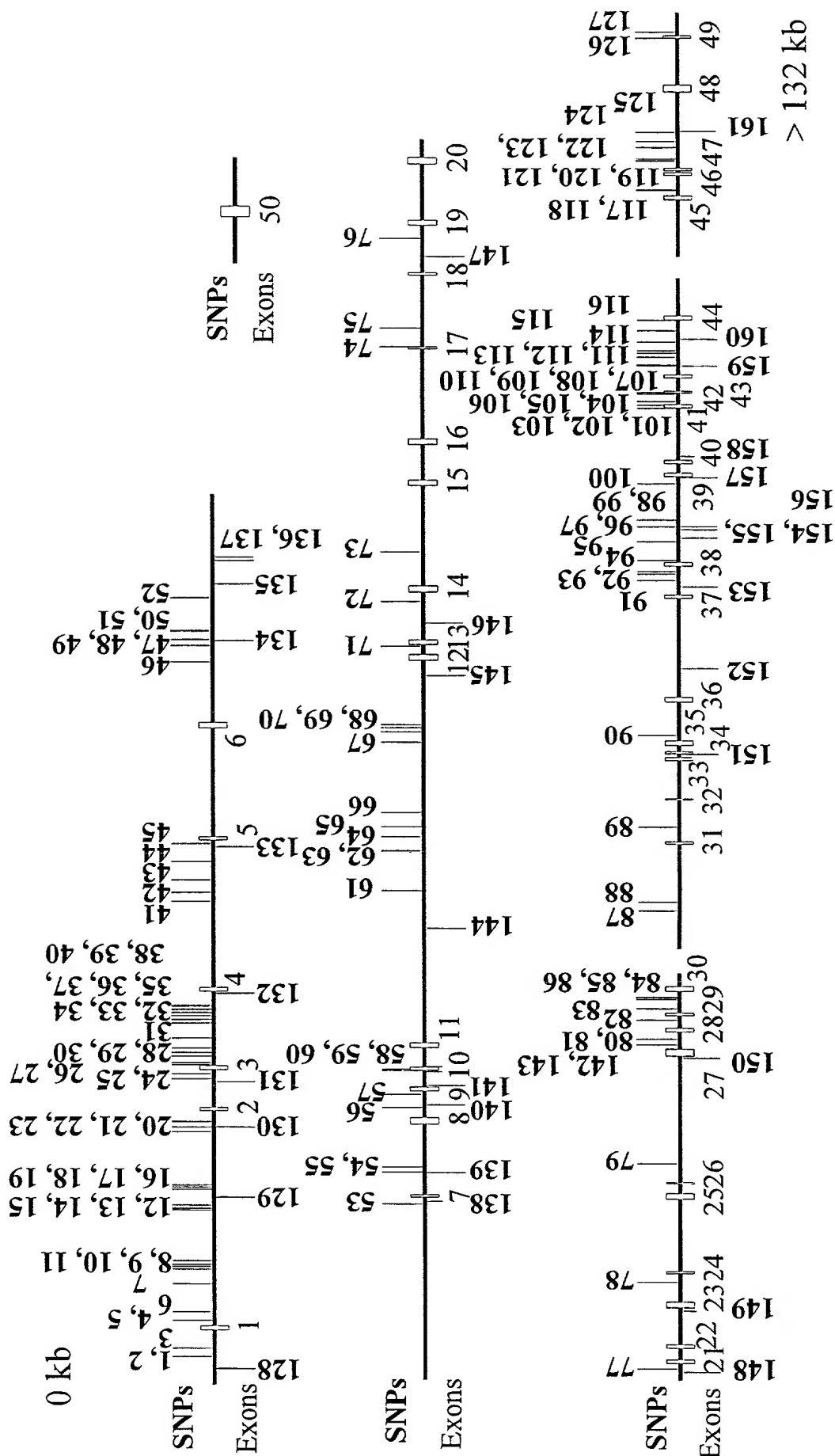


Fig. 146

ATP binding cassette subfamily A, member 7 (ABCA7)

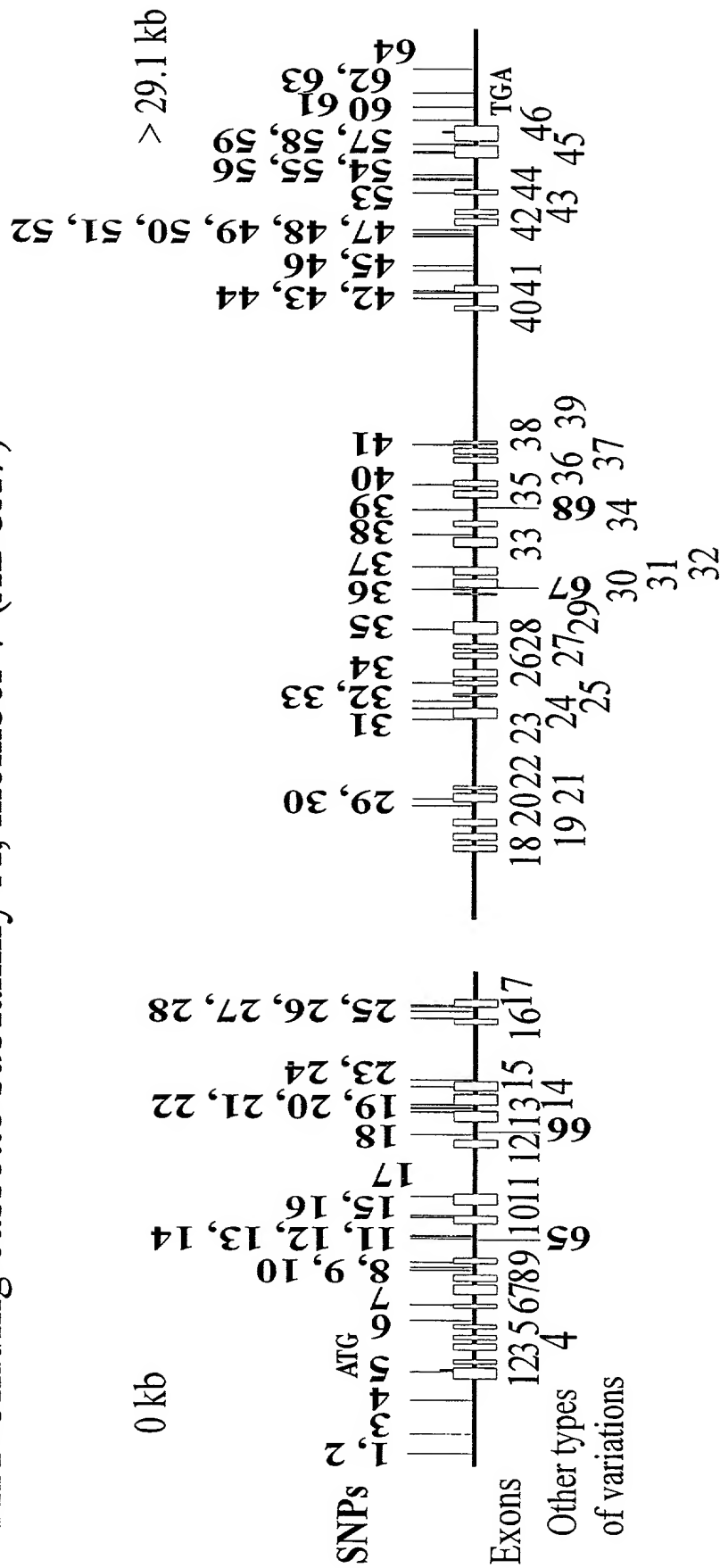


Fig. 147

ATP binding cassette transporter subfamily A member 8 (ABCA8)

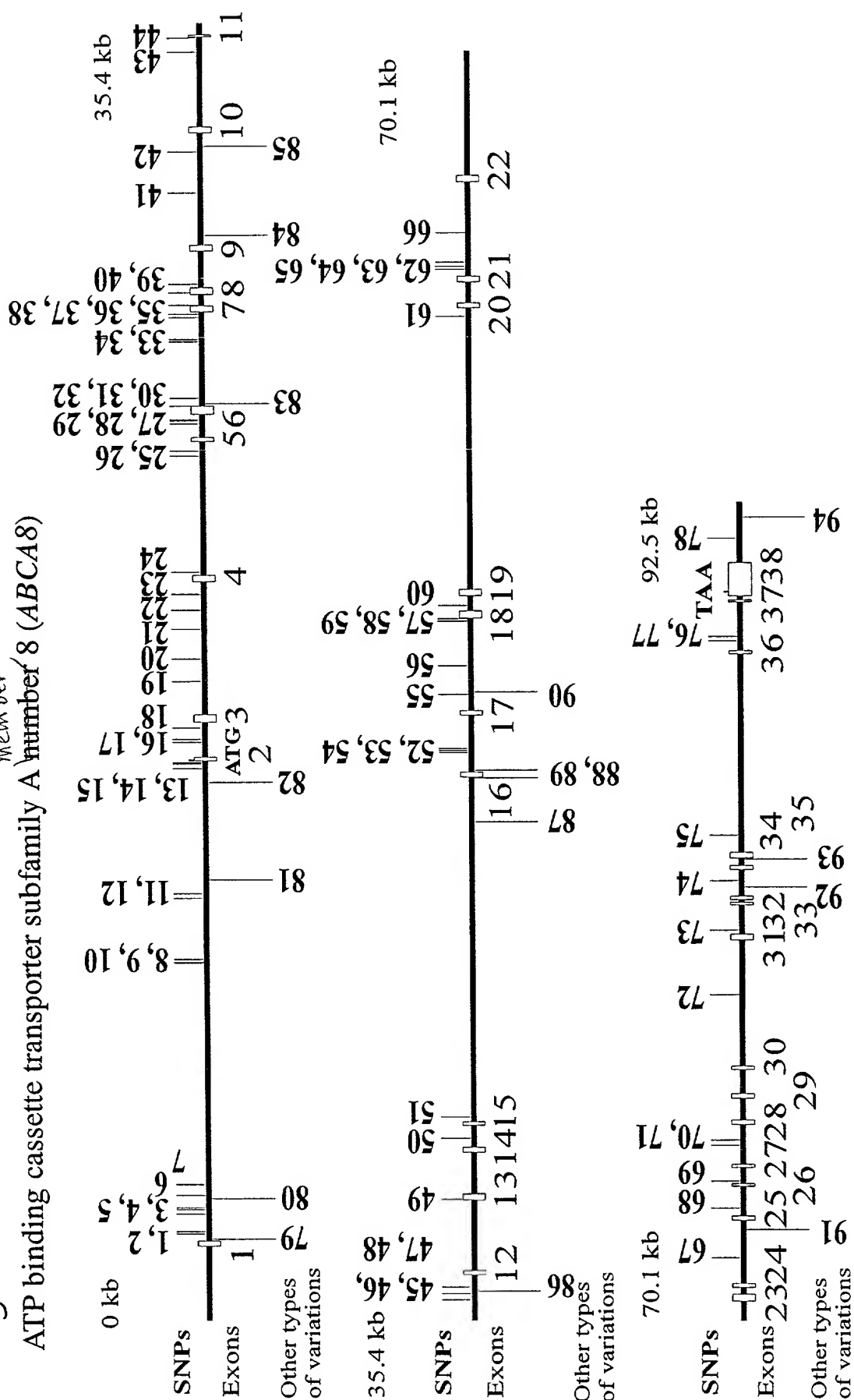


Fig. 148

ATP-binding cassette, sub-family B, member 1 (ABCB1)

ACCESSION AC002457.1
AC005068.1

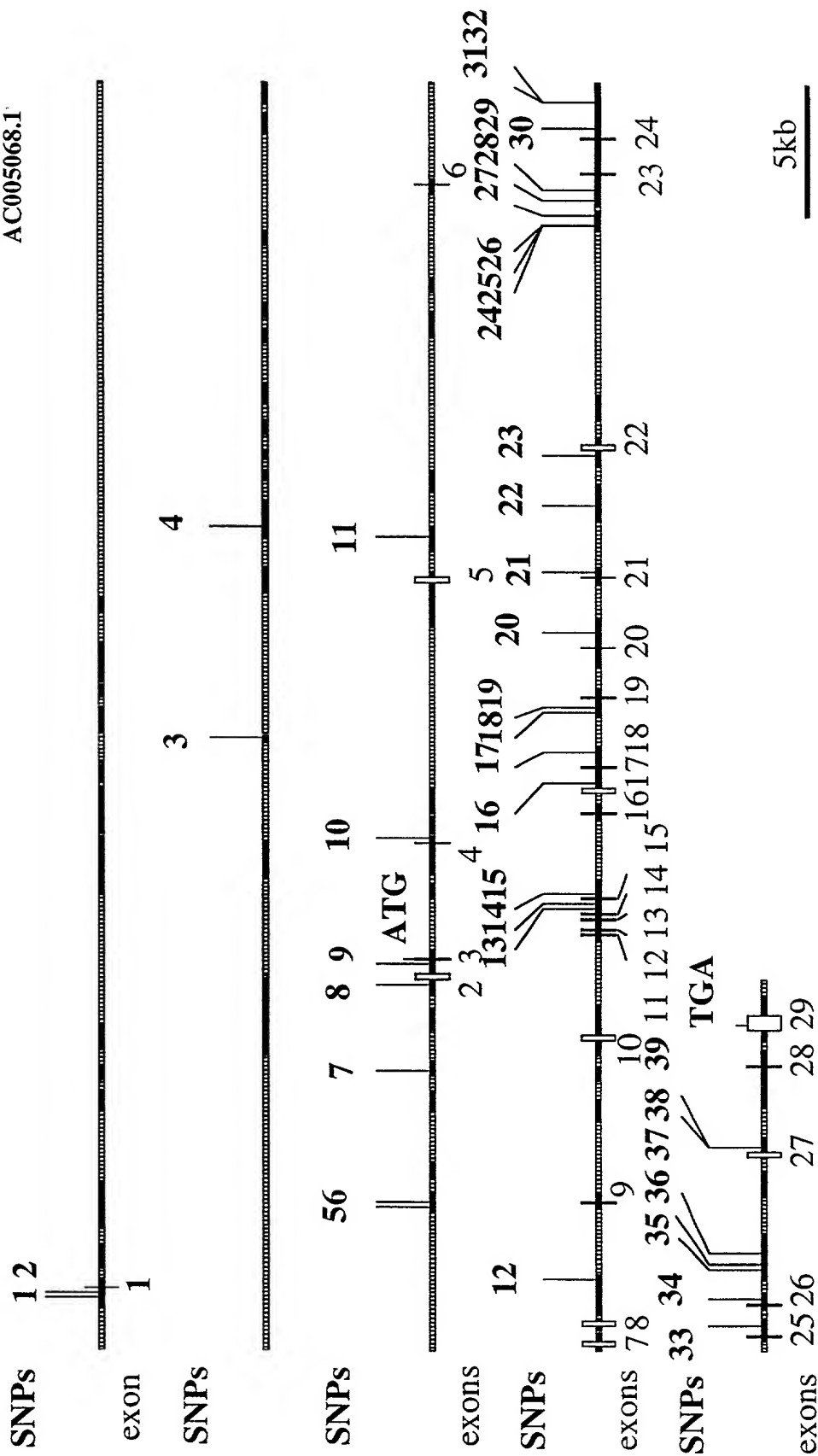


Fig. 149 ATP-binding cassette, sub-family B, member 4 (ABCB4)

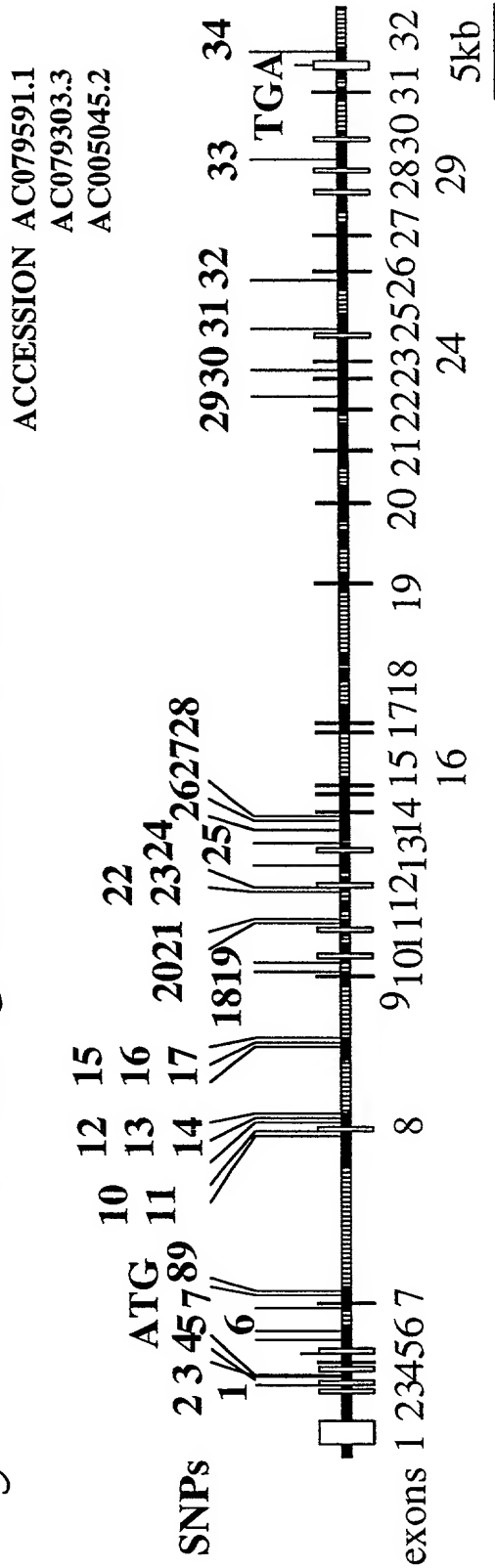


Fig. 150 ATP-binding cassette, sub-family B, member 7 (ABCB7)

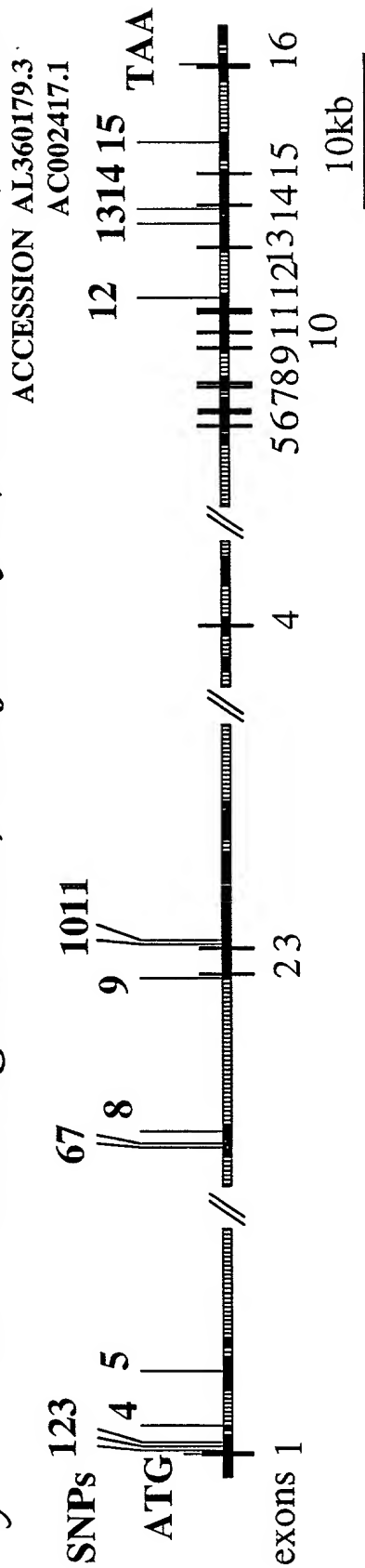


Fig. 151

ATP-binding cassette, sub-family B, member 8 (ABCB8)

ACCESSION AC010973.4

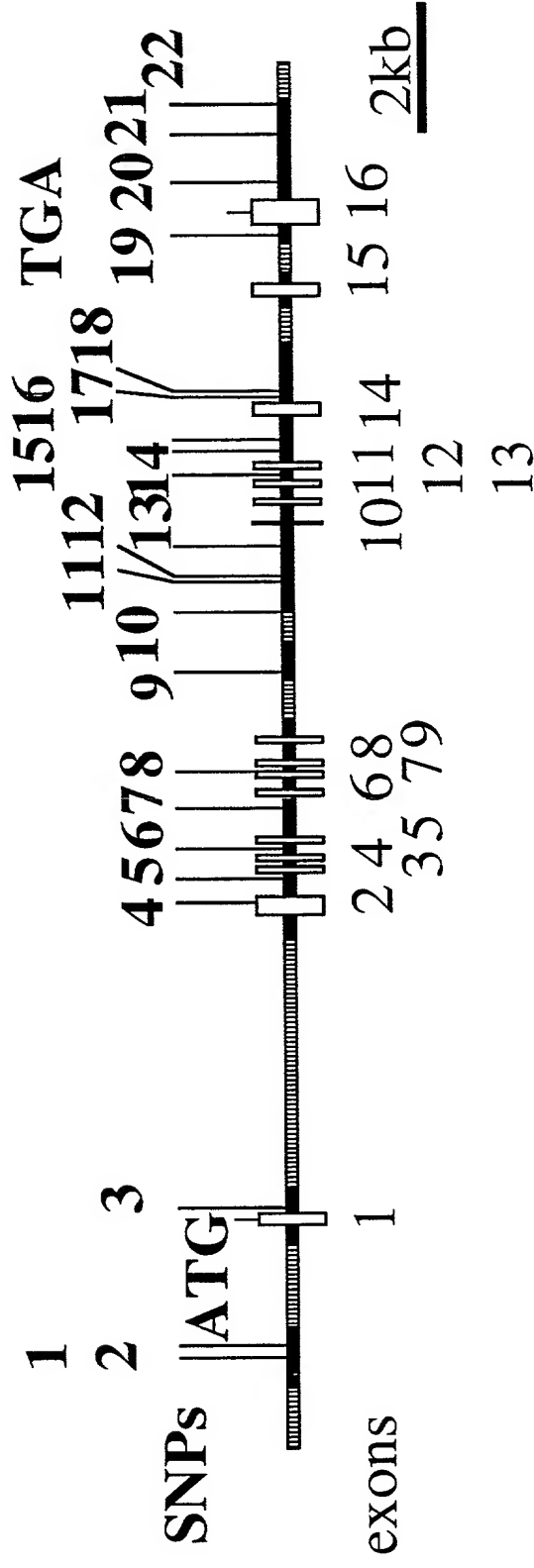


Fig. 152

ATP binding cassette, sub-family B, member 9
(ABCB9)

ACCESSION AC026362.9
AC073857.10

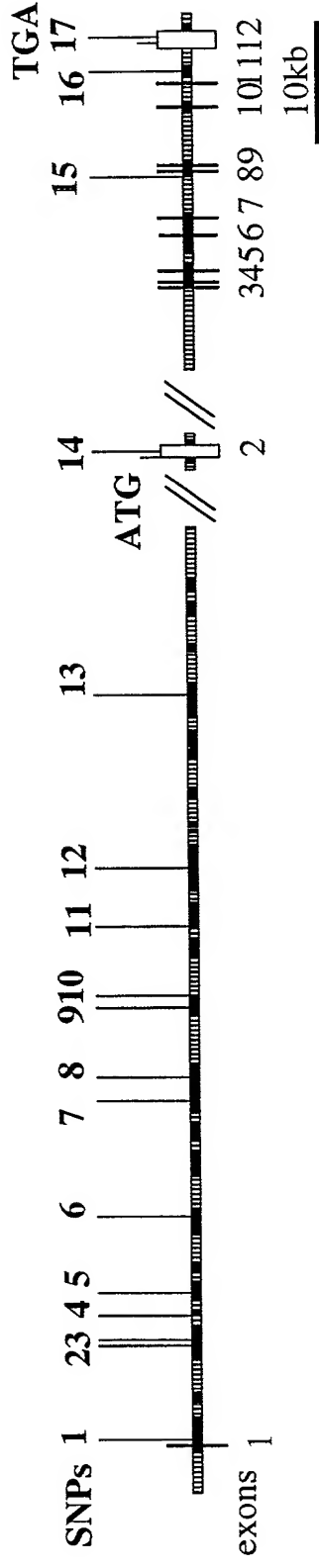


Fig. 153

ATP binding cassette, sub-family B, member 10
(ABCB10)

ACCESSION AL121990.9

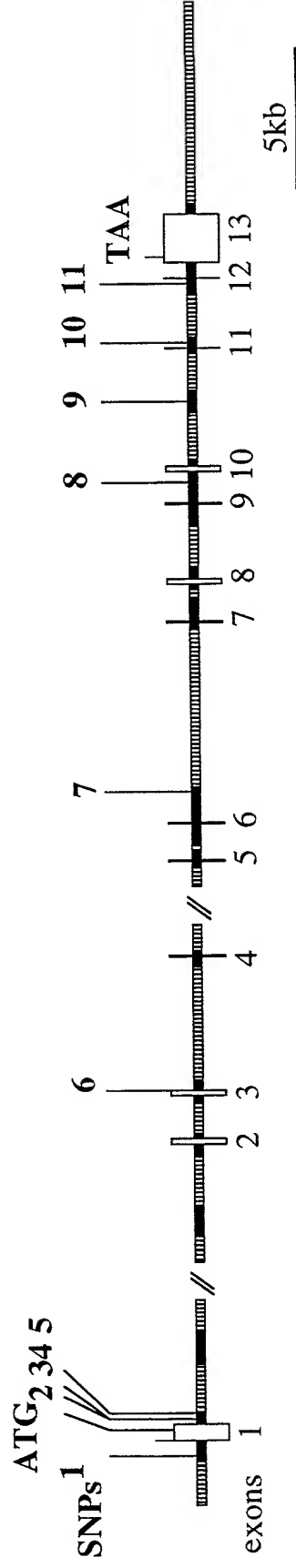


Fig. 254 NADH ubiquinone oxidoreductase 1 alpha subcomplex 1 (NDUFA1)

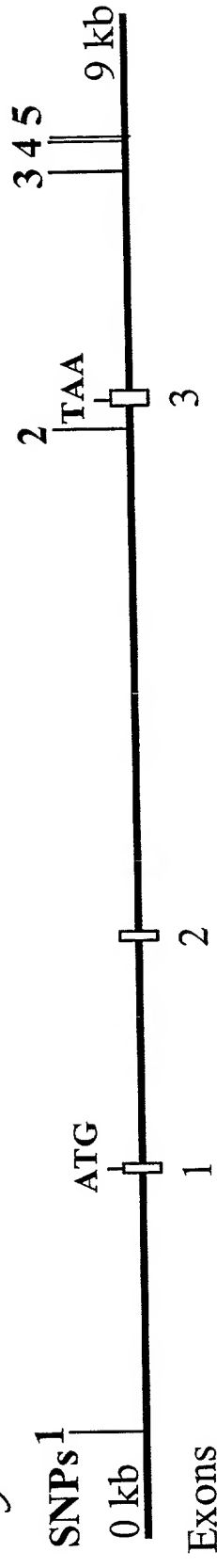


Fig. 255

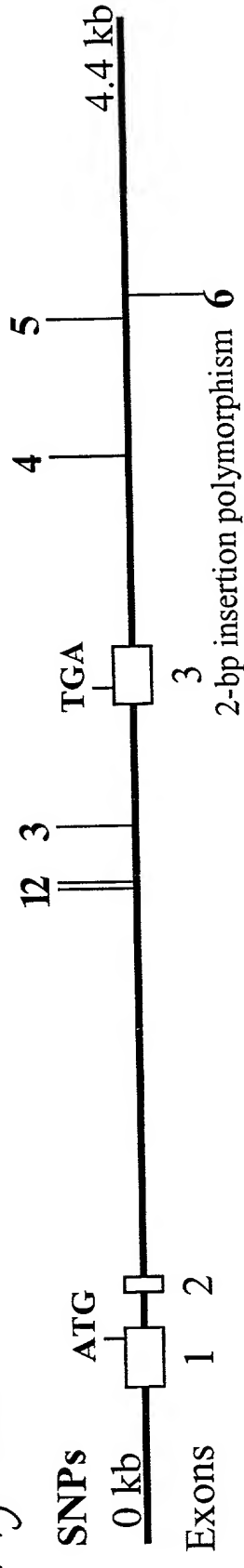


Fig. 256

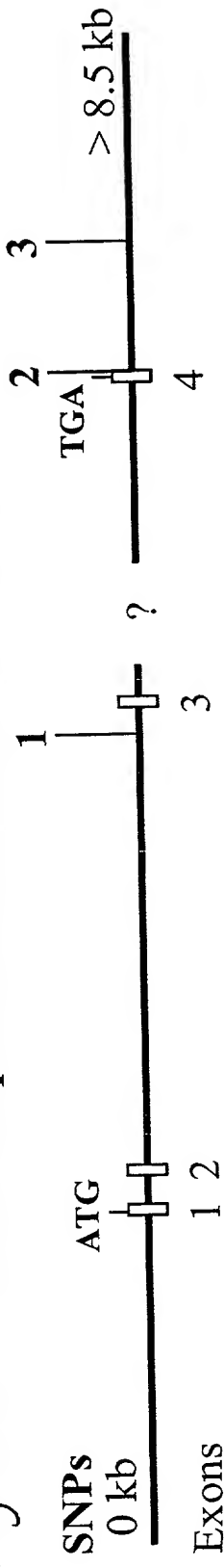


Fig. 155

ATP-binding cassette, sub-family C (CFTR/MRP), member 1

(ABCC1)

ACCESSION AC026452.5
AC025778.4

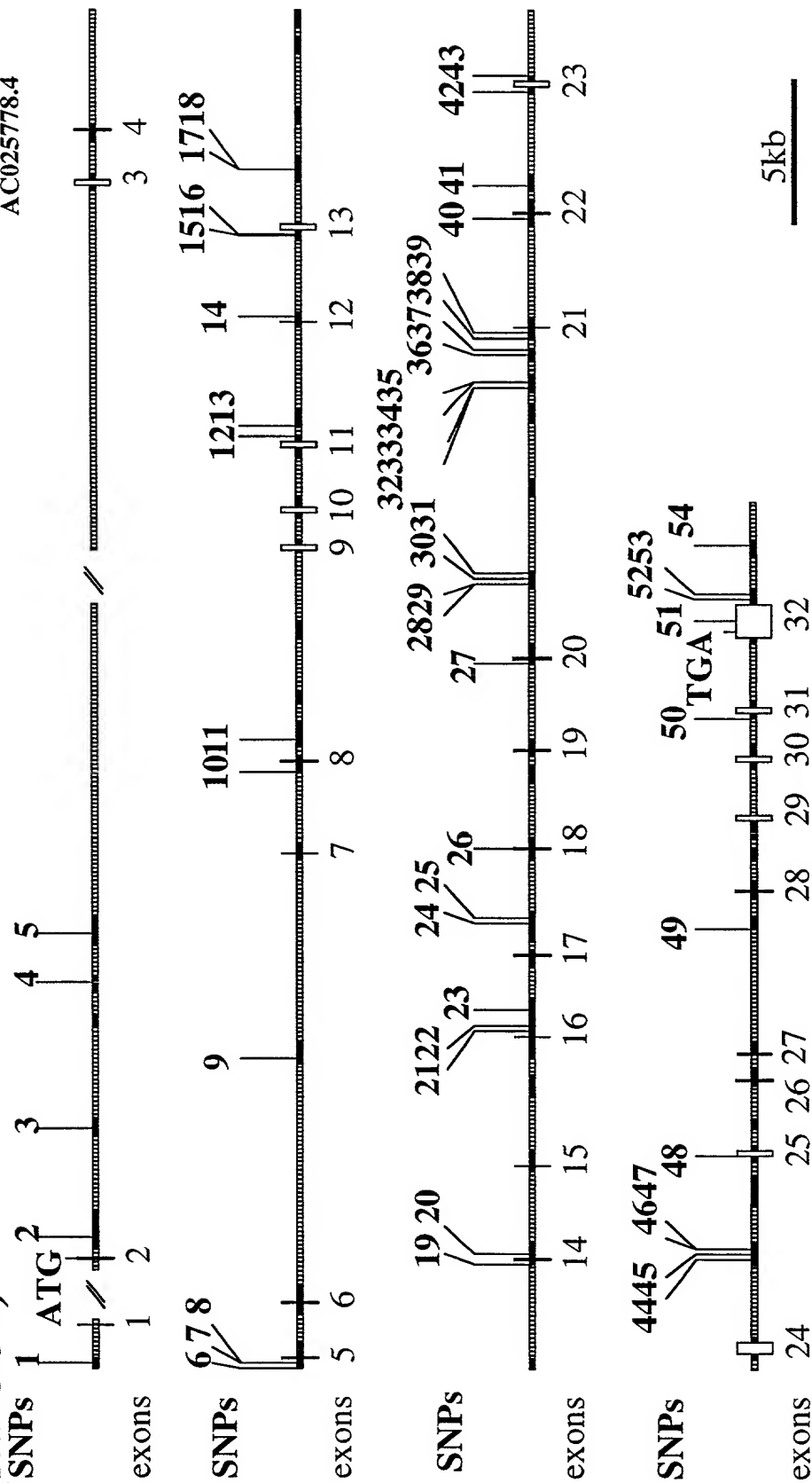


Fig. 157

*ATP-binding cassette, sub-family C
(CFTR/MRP), member 3 (ABCC3)*

ACCESSION AC004590.1
AC005921.3

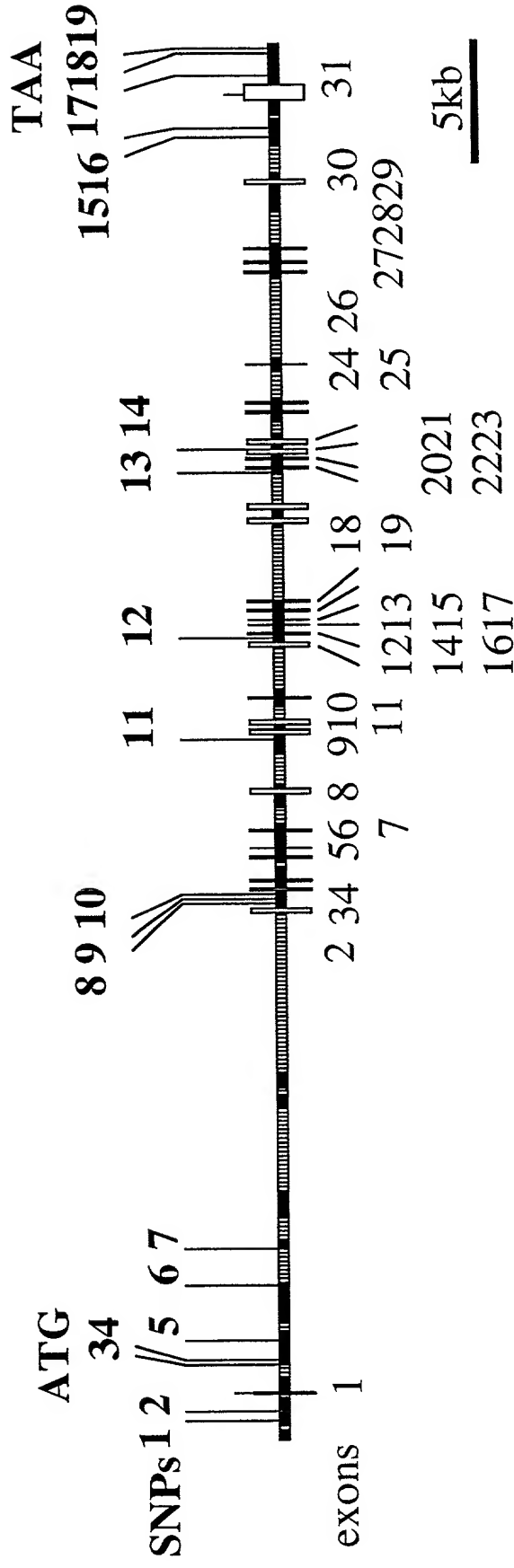


Fig. 158A *ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4)*

ACCESSION AL356257.11 AL157818.12 AL139381.12

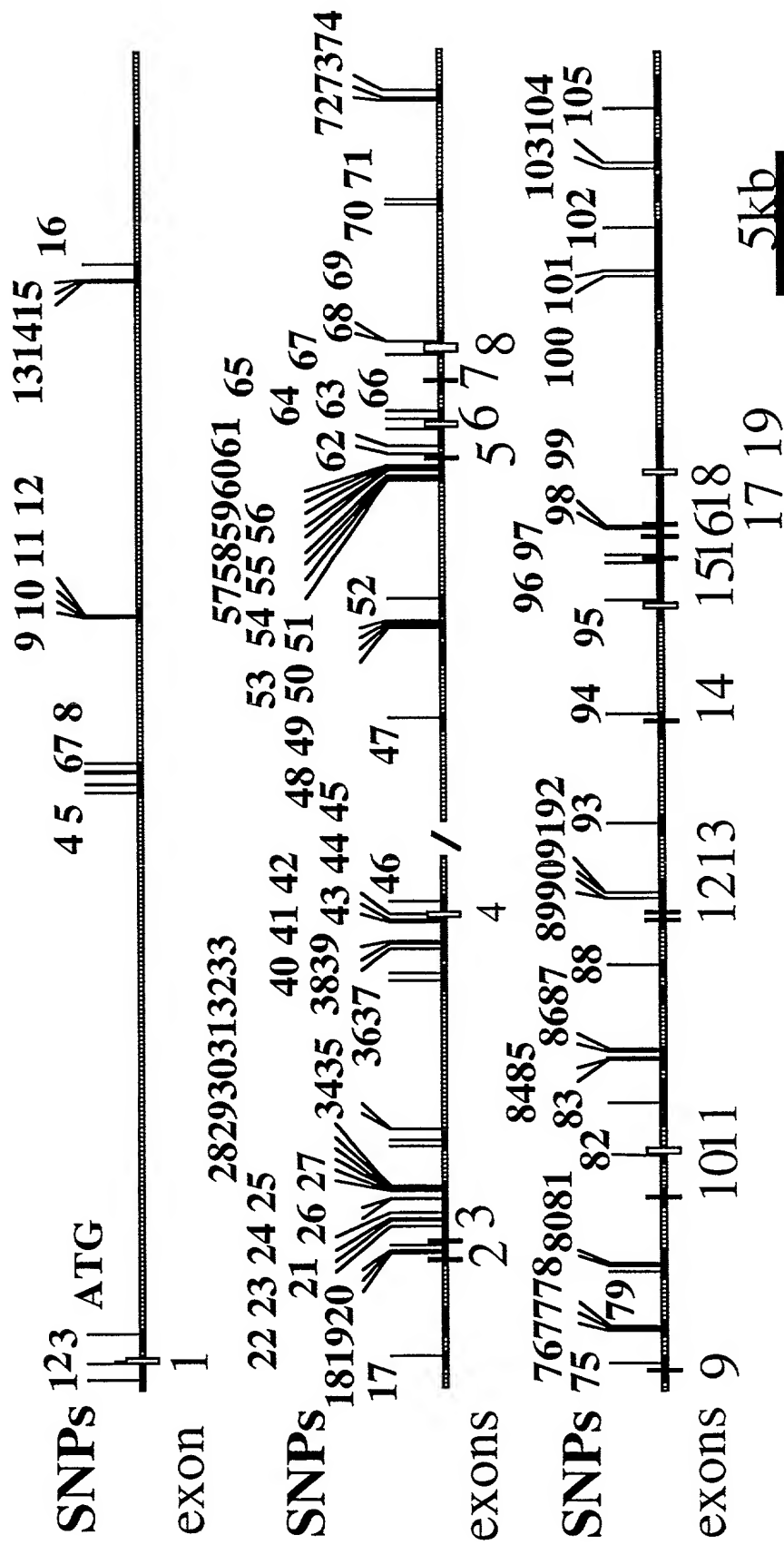


Fig. 158B

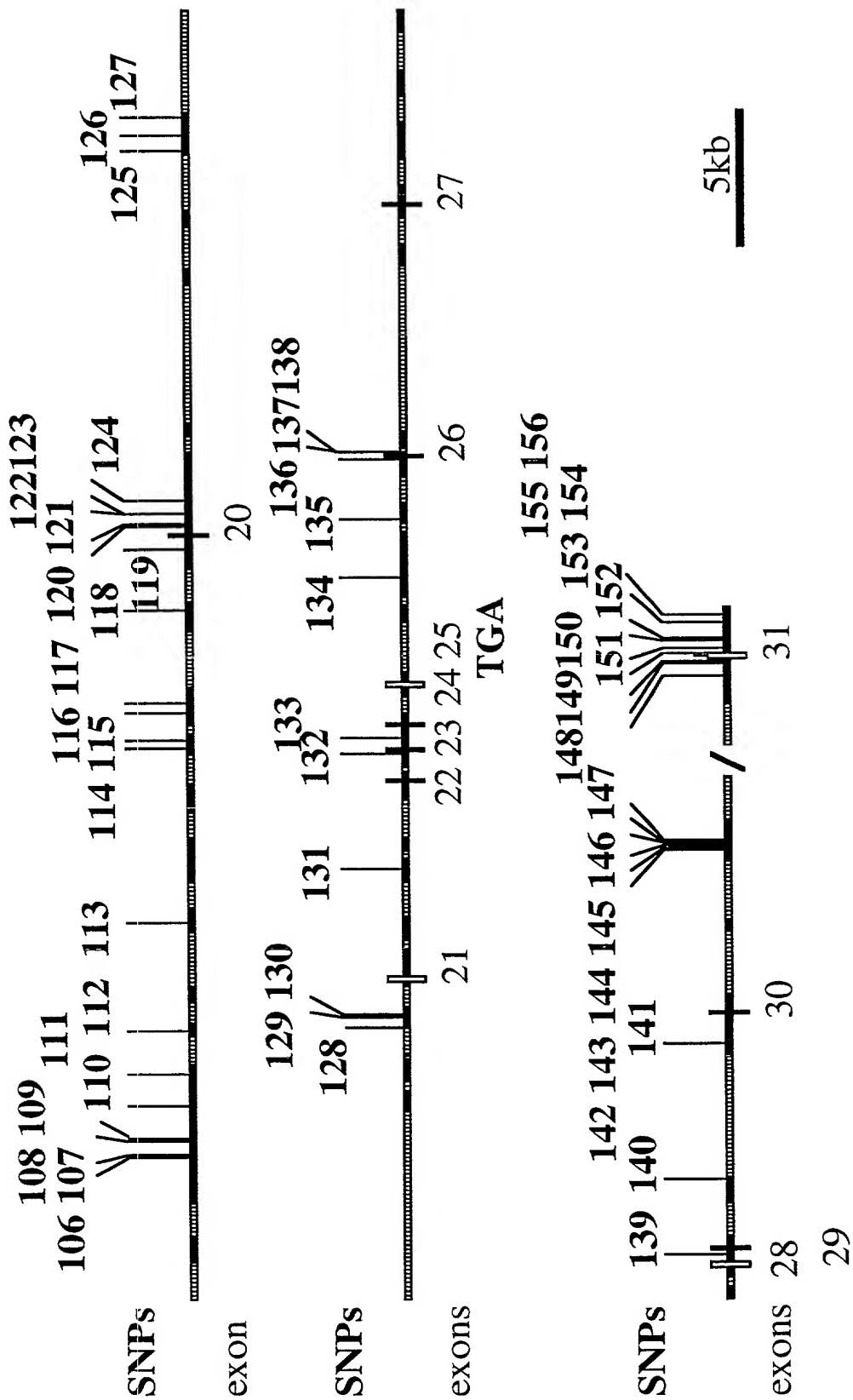


Fig. 159 ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)

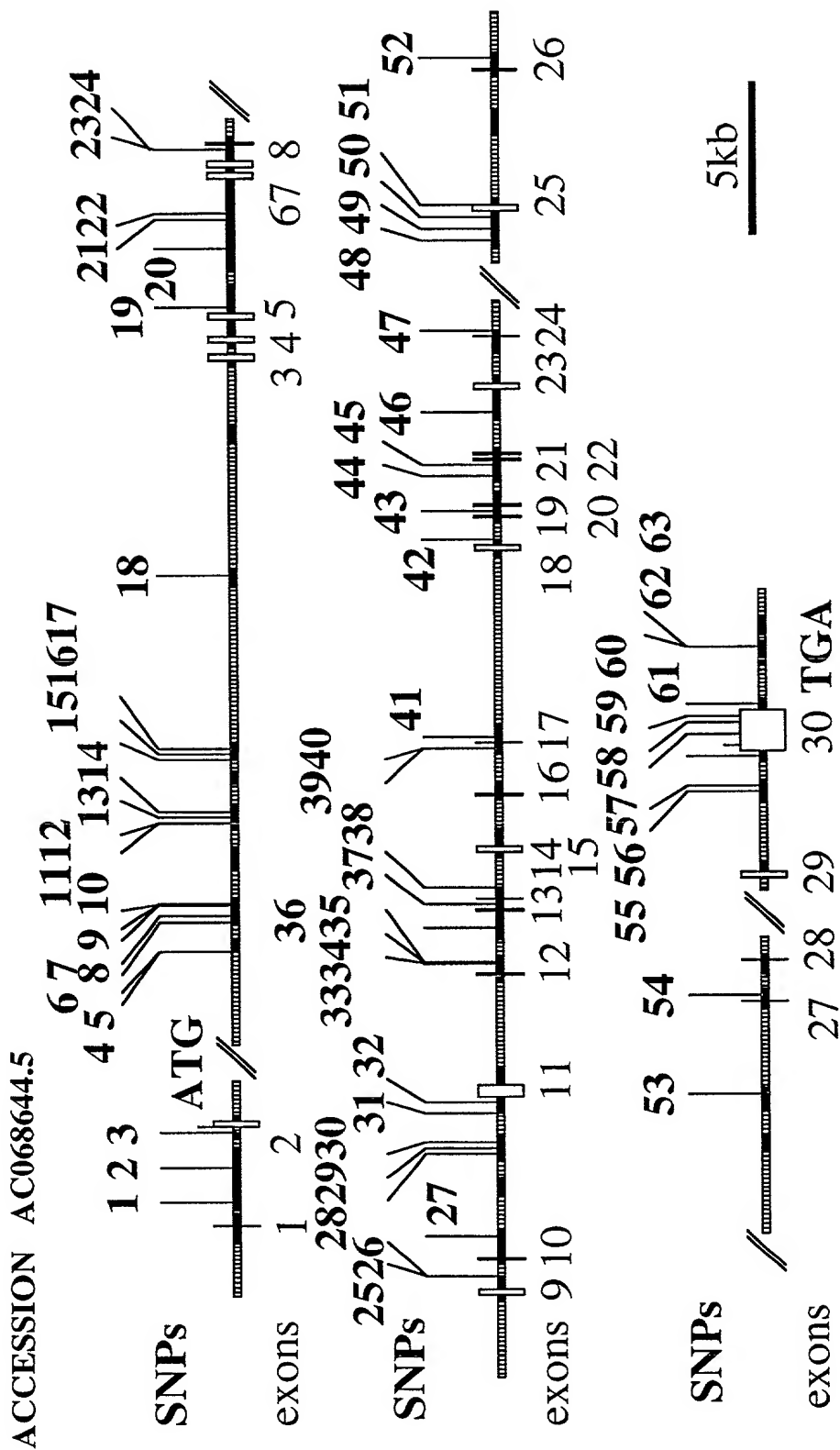


Fig. 160 ATP binding cassette, sub-family C (CFTR/MRP), member 7 (ABCC7)

ACCESSION AC000111.1 AC000061.1

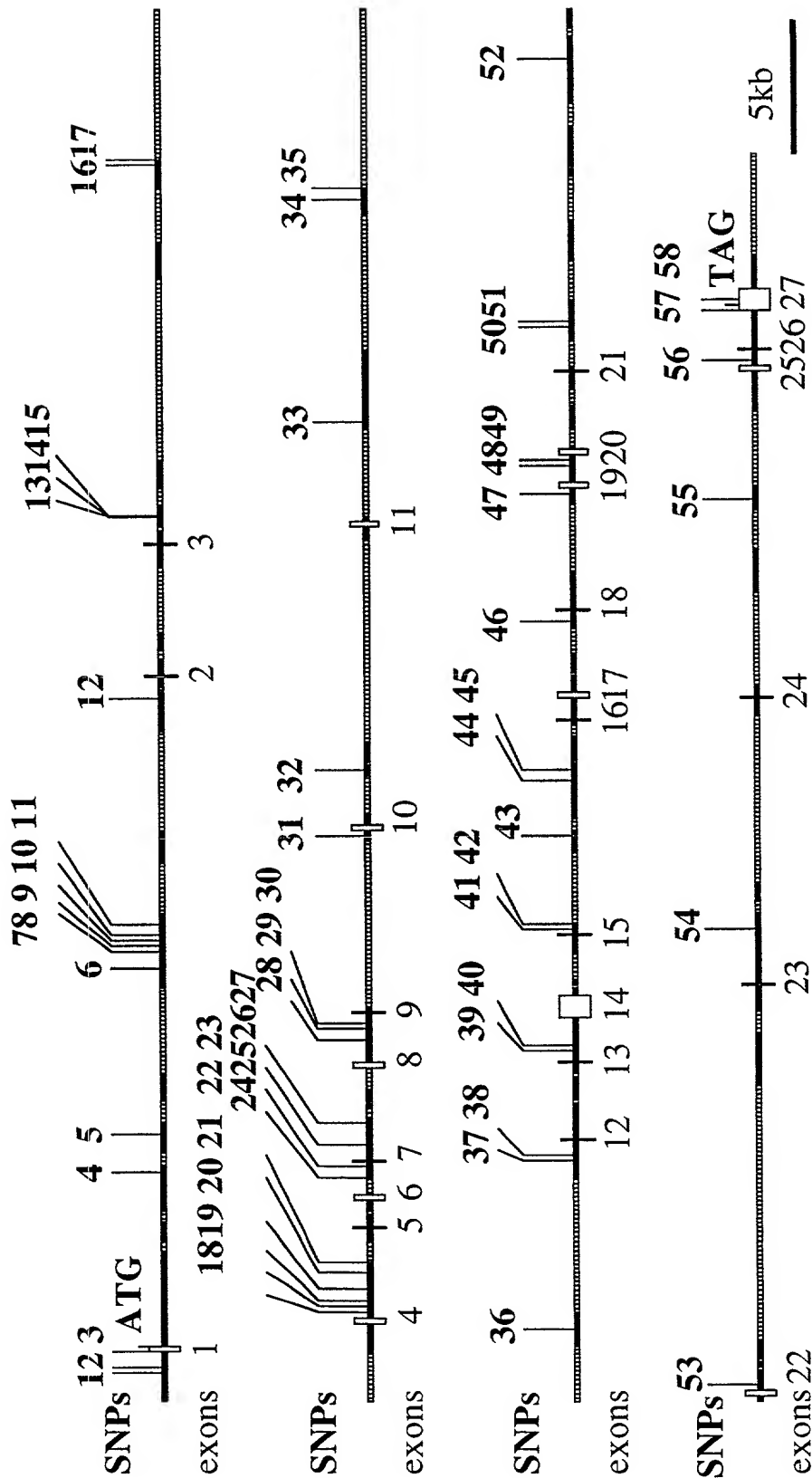


Fig. 161 ATP binding cassette, sub-family C (CFTR/MRP), member 8 (ABCC8)

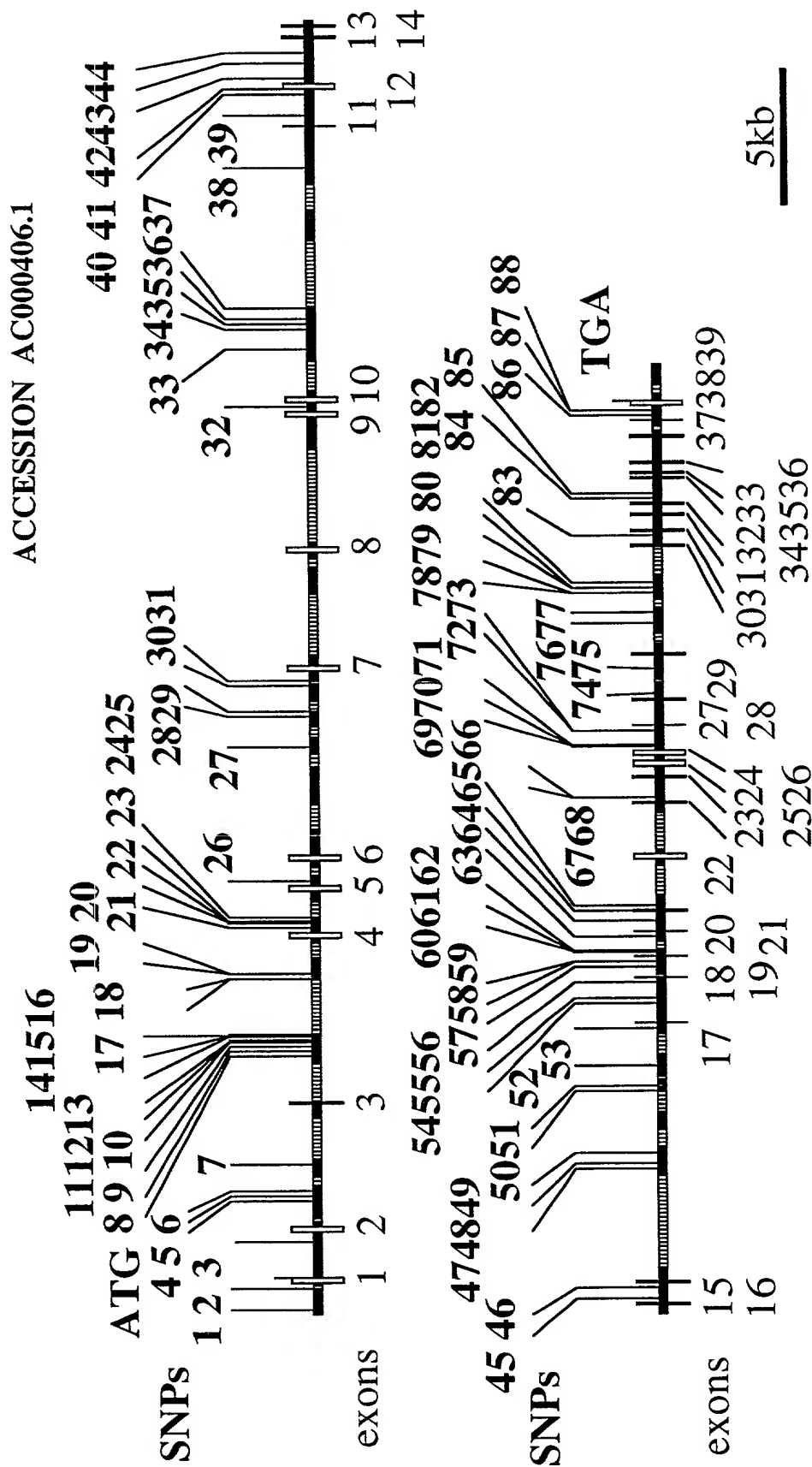


Fig. 162 ATP binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9)

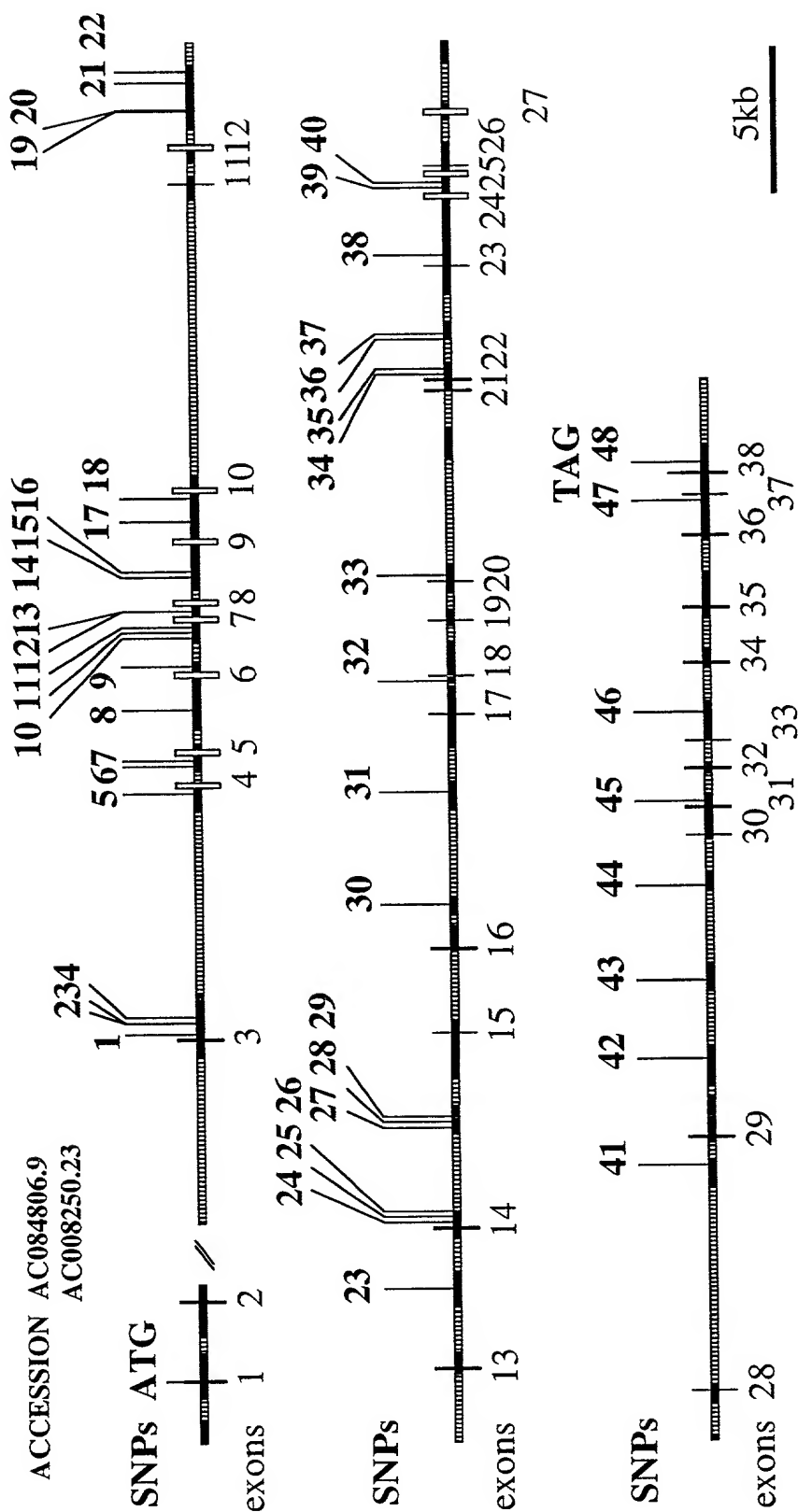


Fig. 163

ATP binding cassette subfamily D, member 1 (*ABCD1*)

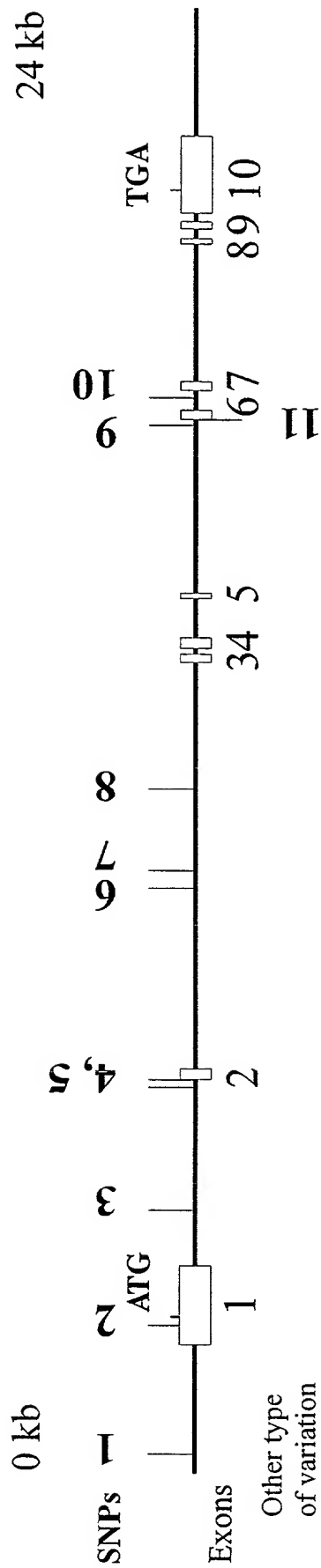


Fig. 164

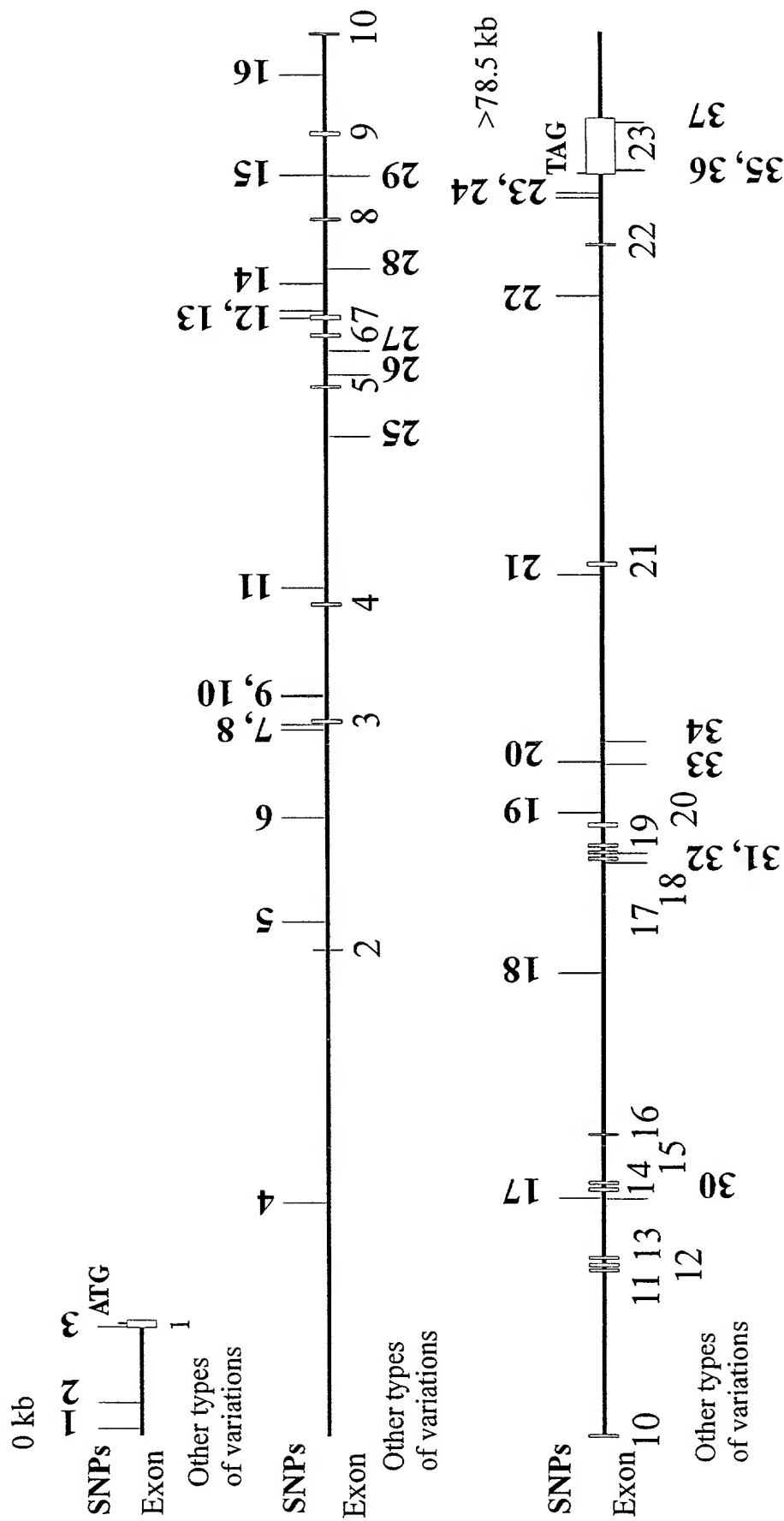
ATP binding cassette subfamily D, member 3 (*ABCD3*)

Fig. 165

ATP binding cassette subfamily D, member 4 (*ABCD4*)

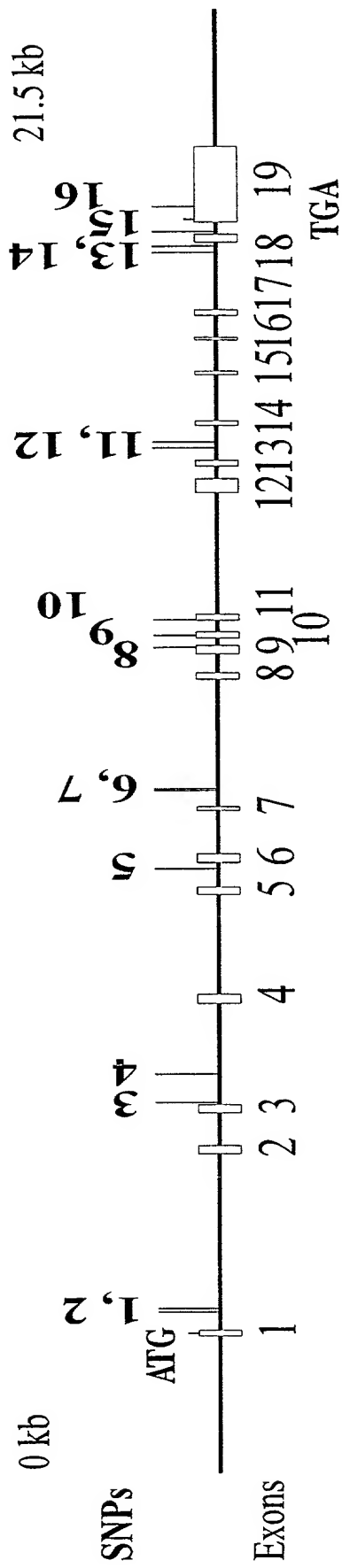


Fig. 166

ATP binding cassette subfamily G, member 1 (ABCG1)

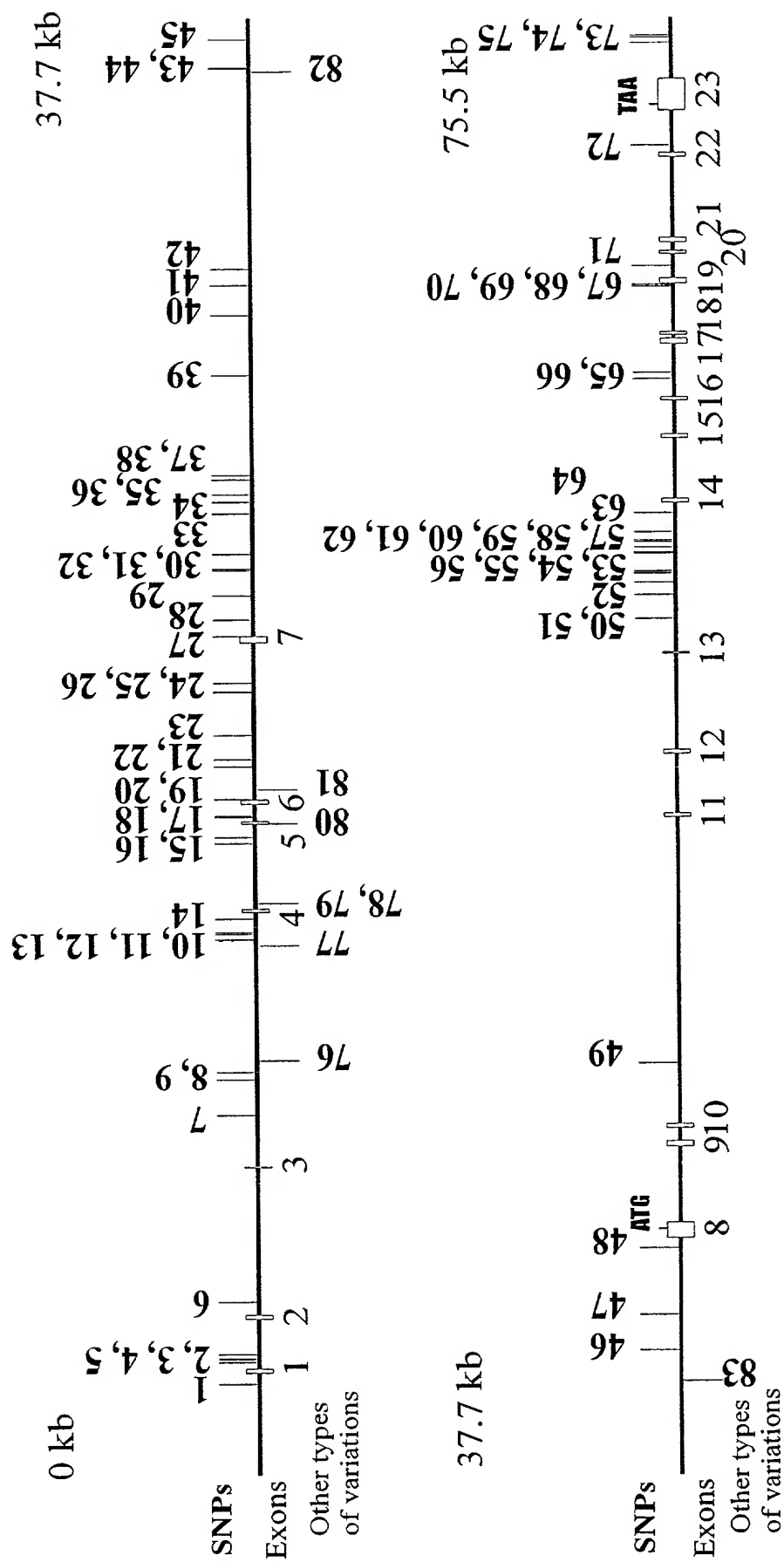


Fig. 167

ATP binding cassette subfamily G, member 2 (*ABCG2*)

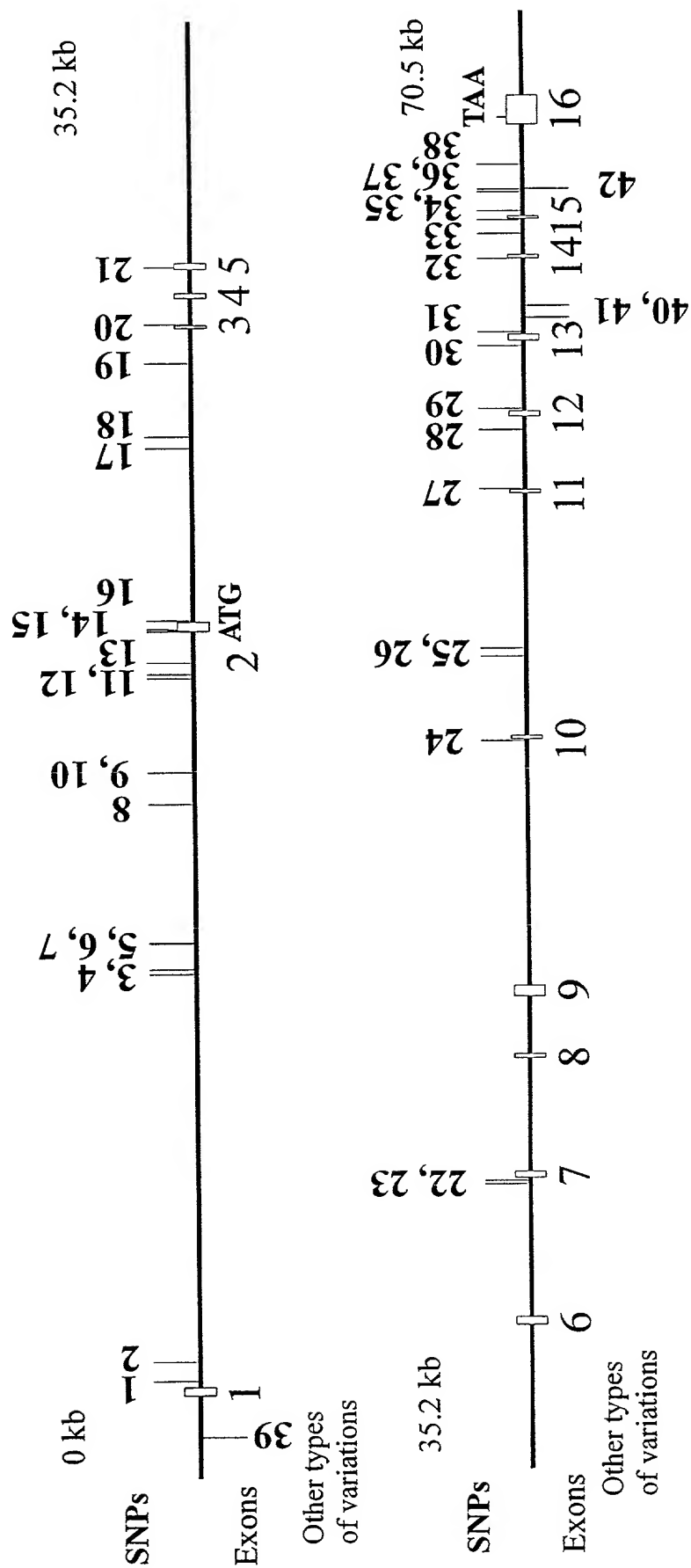


Fig. 168

ATP binding cassette, subfamily G, member 4 (*ABCG4*)

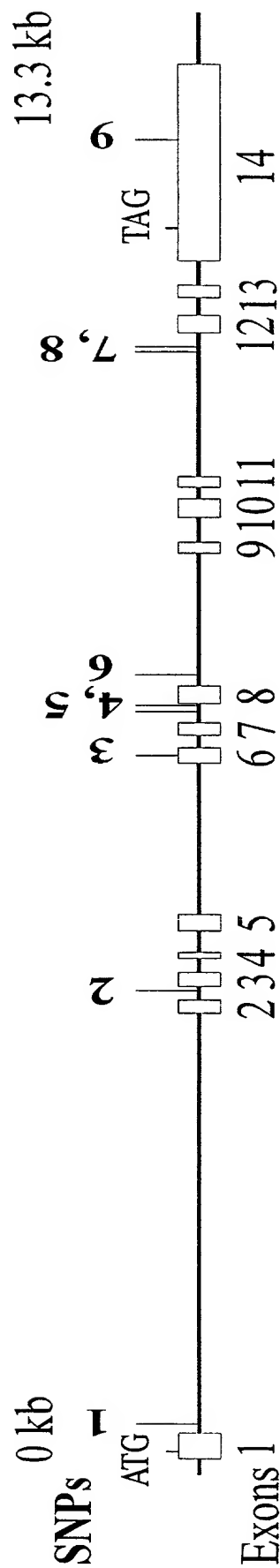


Fig. 170

ATP binding cassette transporter subfamily G number 8 (ABCG8)

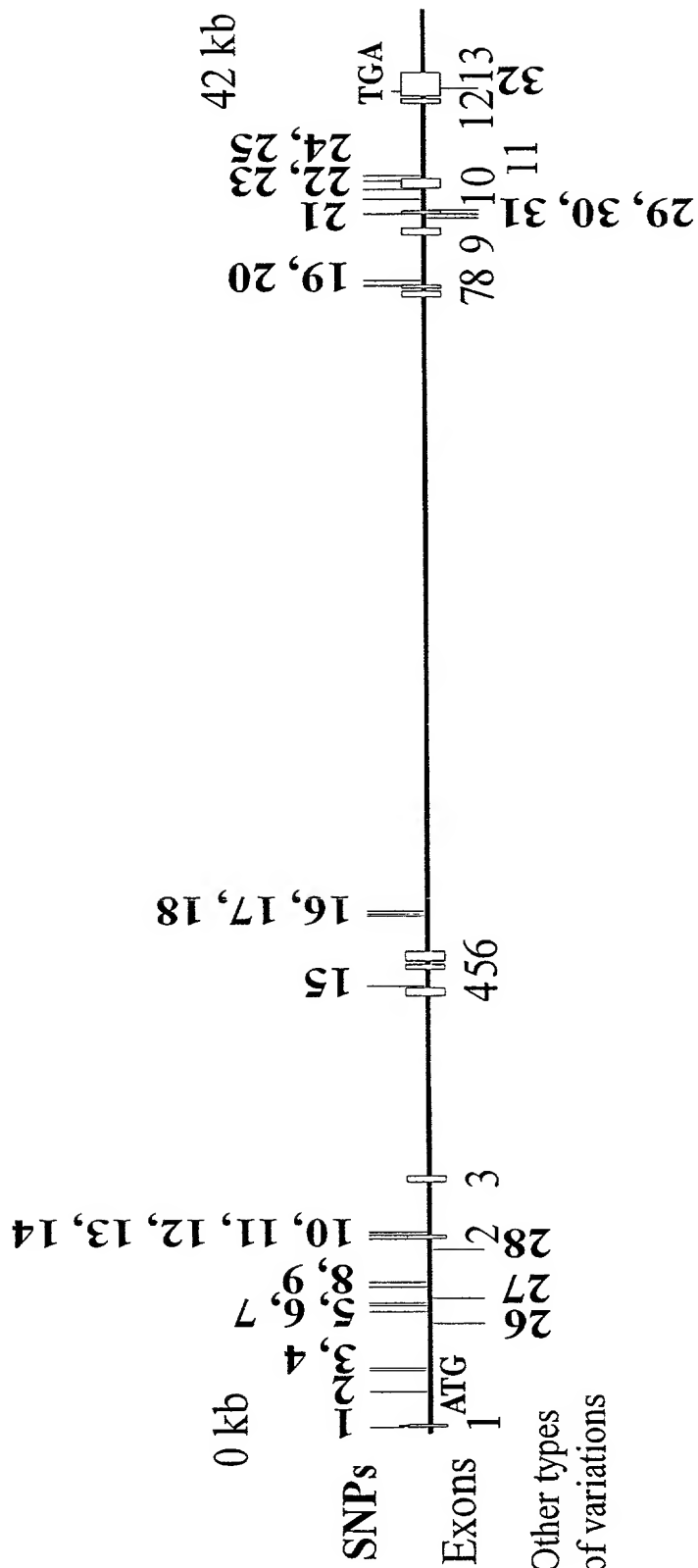


Fig. 171

ATP binding cassette subfamily E, member 1 (*ABCE1*)

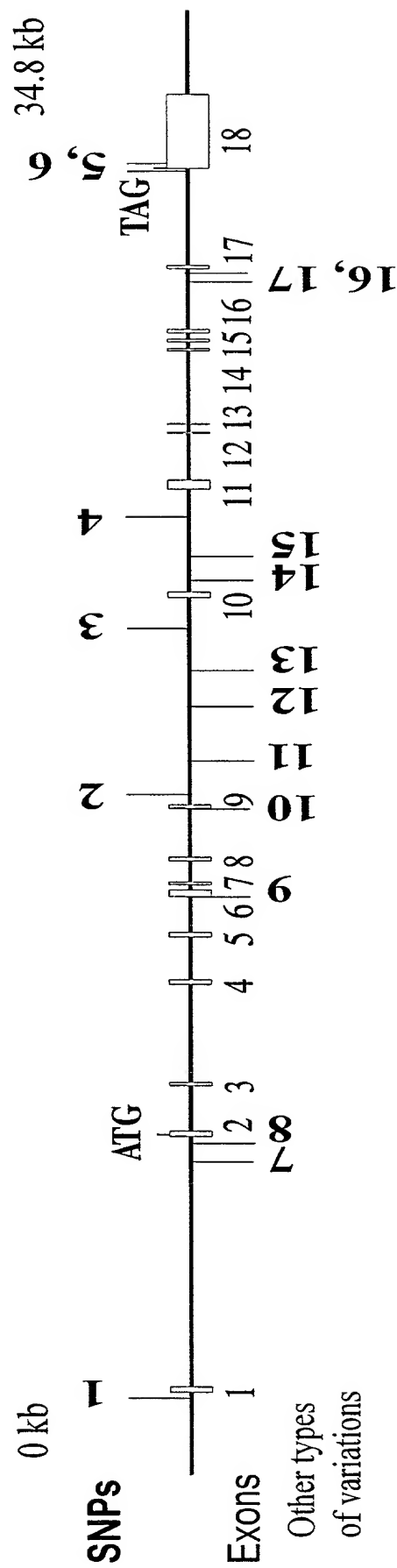


Fig. 172

ATP binding cassette superfamily ^{sub}member 1 (*ABCF1*)

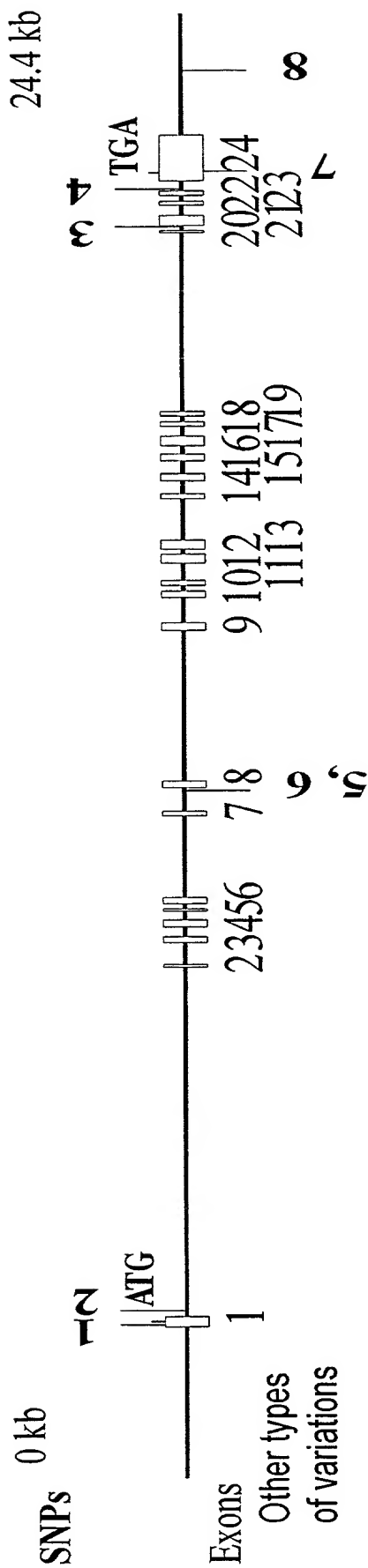


Fig. 173

Human organic anion transporter 1 (*hOAT1*)

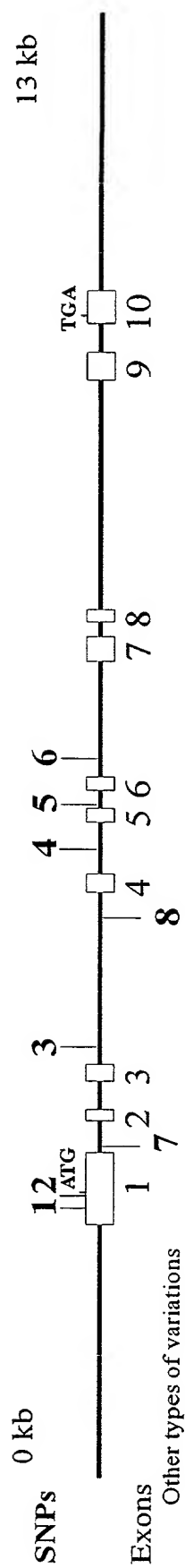


Fig. 174

Human organic anion transporter 2 (*hOAT2*)

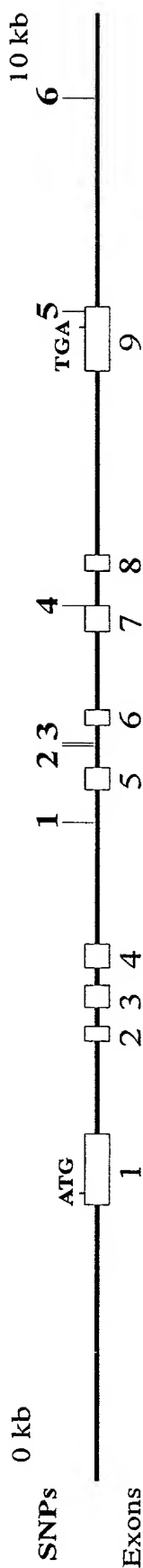


Fig. 175

Human organic anion transporter 3 (*hOAT3*)

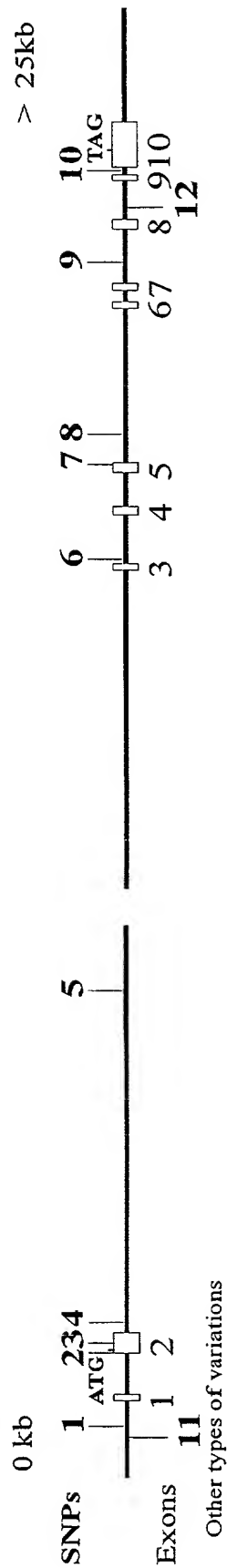


Fig. 176

Human organic anion transporting polypeptide 1 (*hOATP1*)

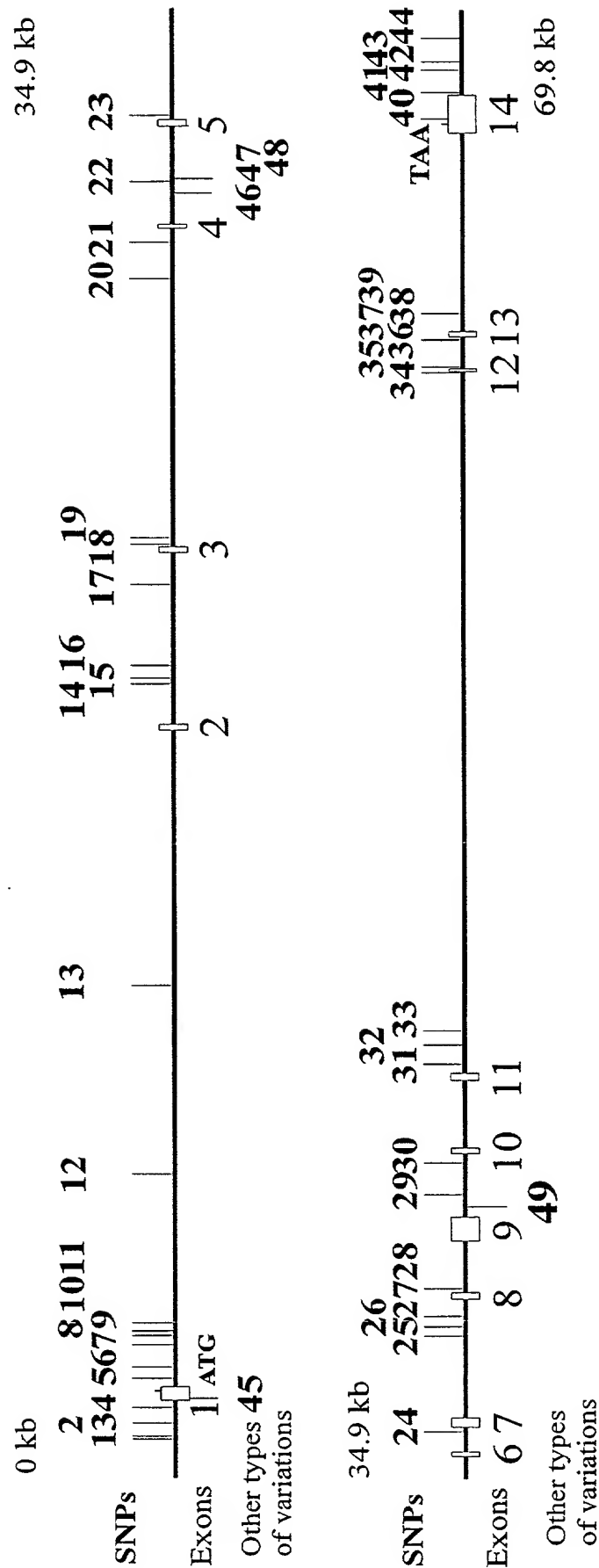


Fig. 177

Human organic anion transporting polypeptide 2 (*hOATP2*)

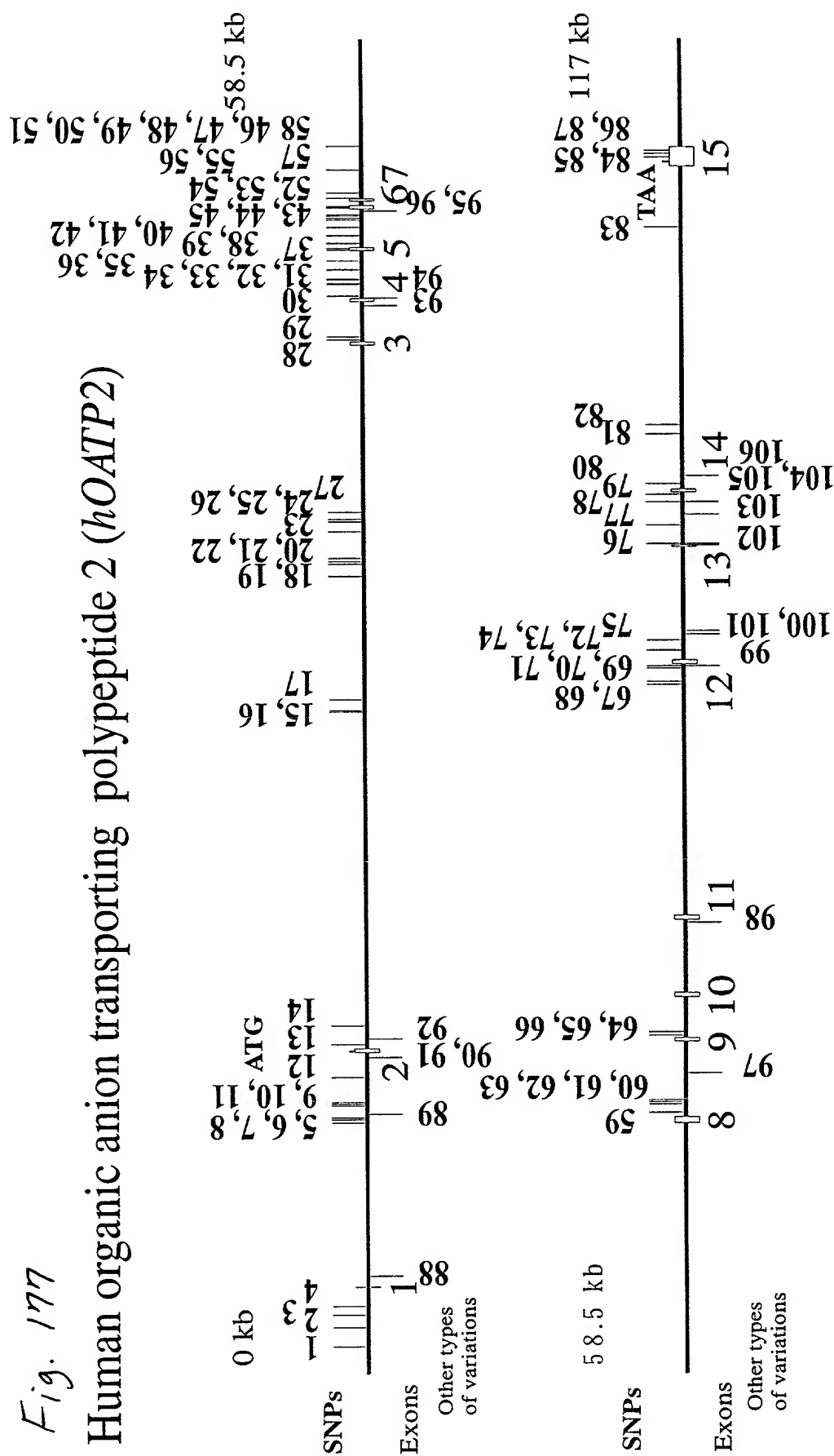


Fig. 178

Human organic anion transporting polypeptide 8 (*hOATP8*)

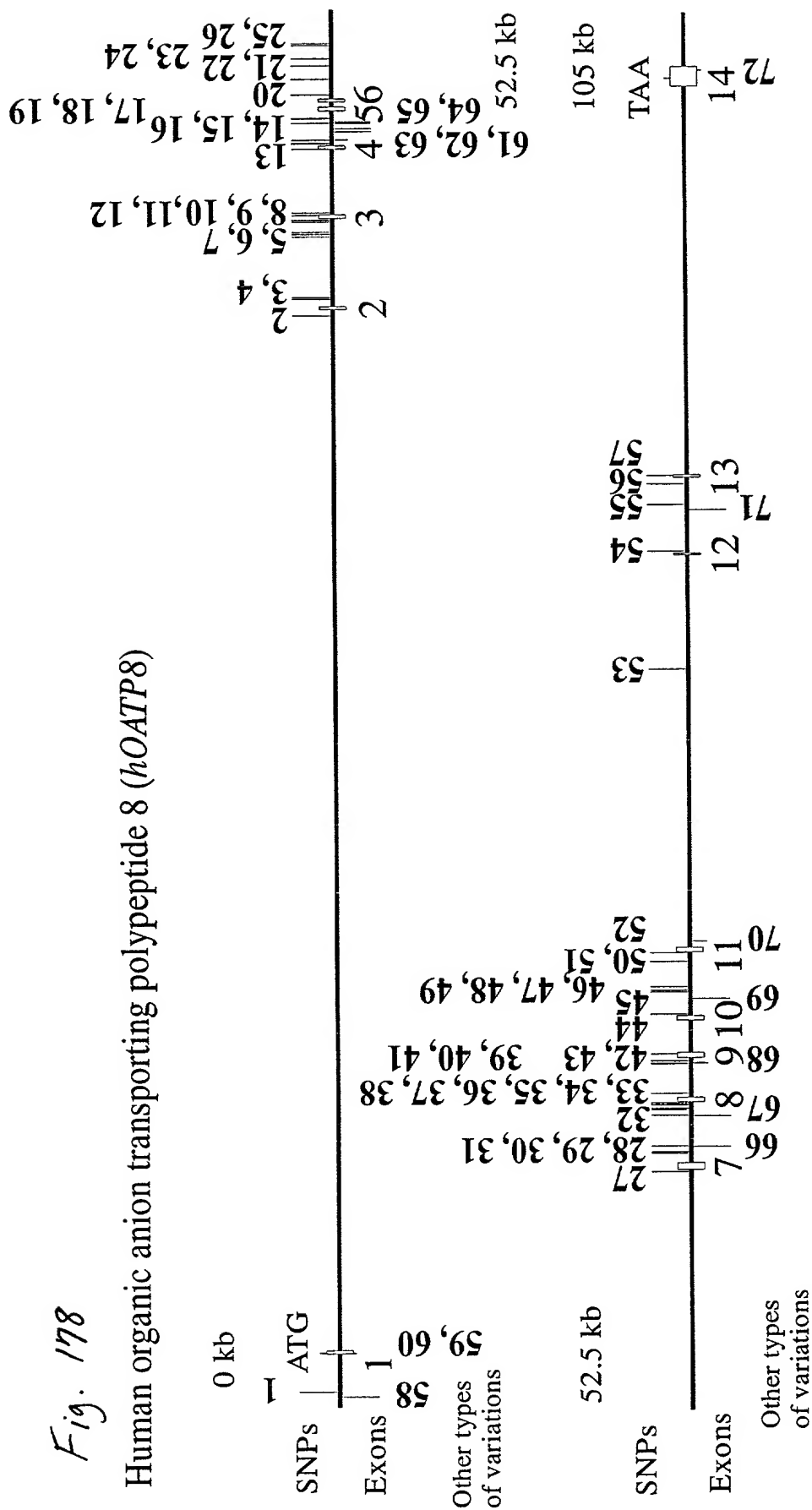


Fig. 179 *Transporter associated with antigen processing 1 (TAP1)*

ACCESSION X66401.1

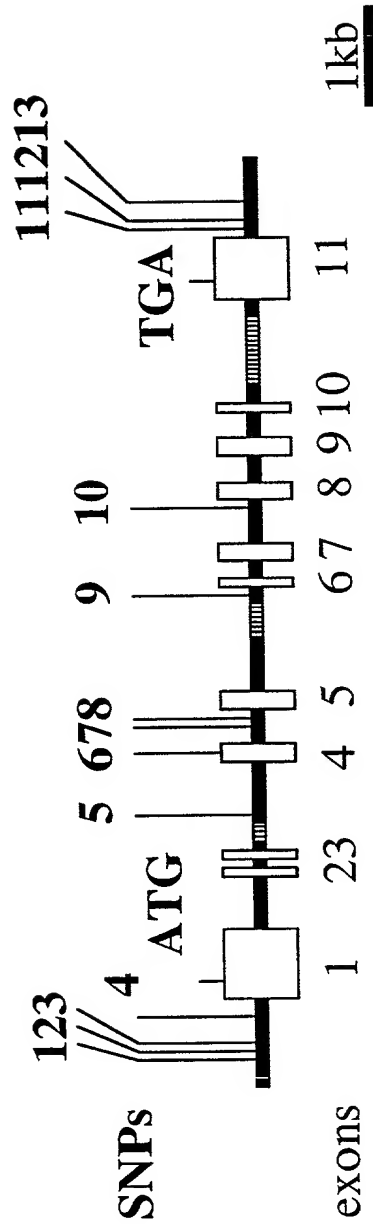


Fig. 180 *Transporter associated with antigen processing 2 (TAP2)*

ACCESSION X66401.1

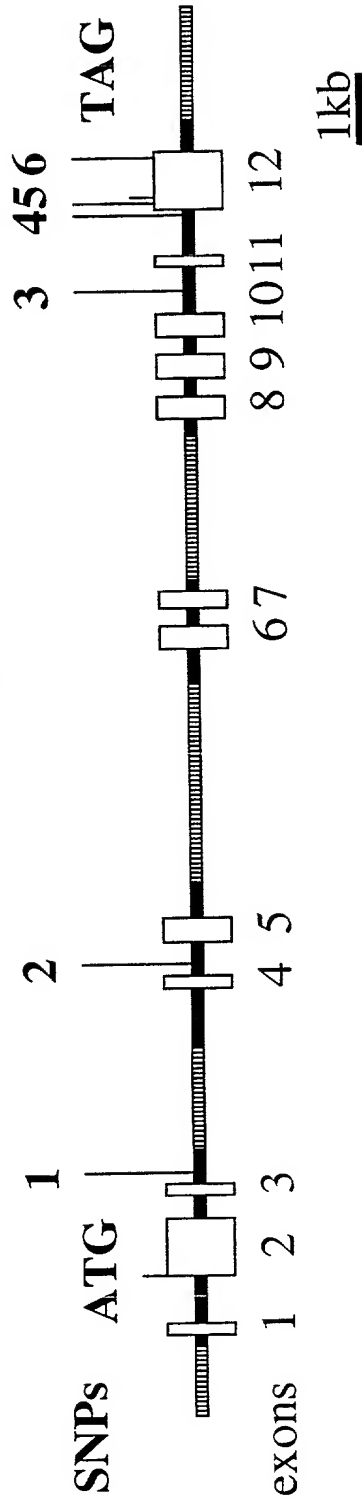


Fig. 181

Solute carrier family 22, member 4 (SLC22A4)
Organic cation transporter, member 4 (OCTN1)

ACCESSION AC008599.6

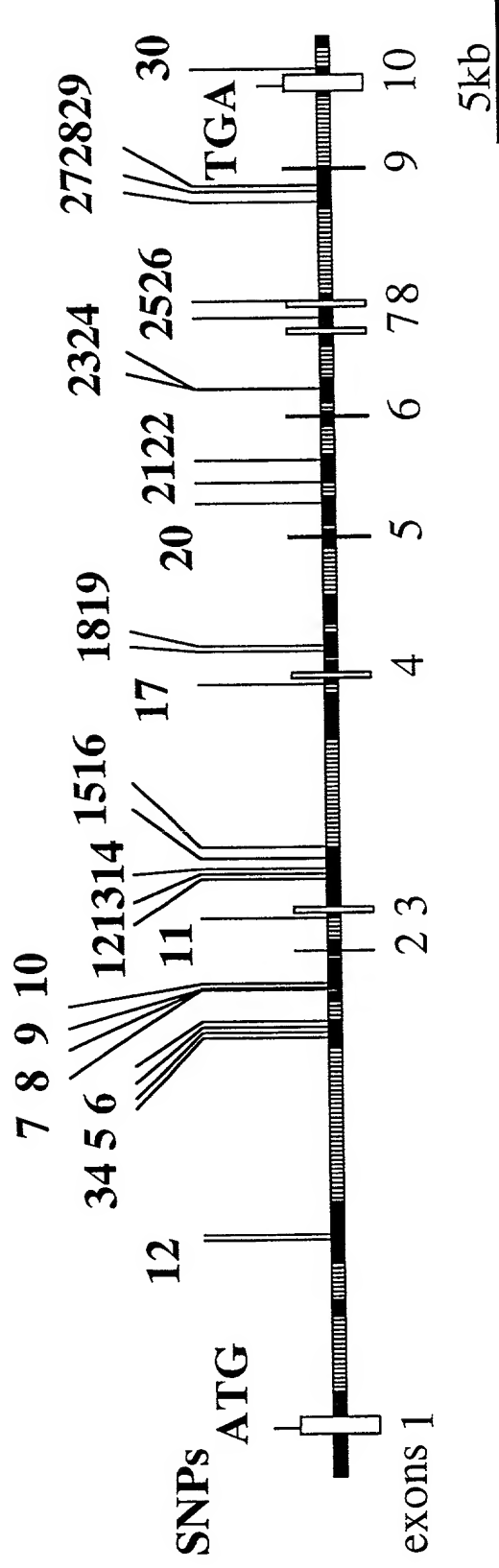


Fig. 182

Solute carrier family 22, member 5 (SLC22A5)
Organic cation transporter, member 5 (OCTN2)

ACCESSION AC023861.3

ATG
 123 45

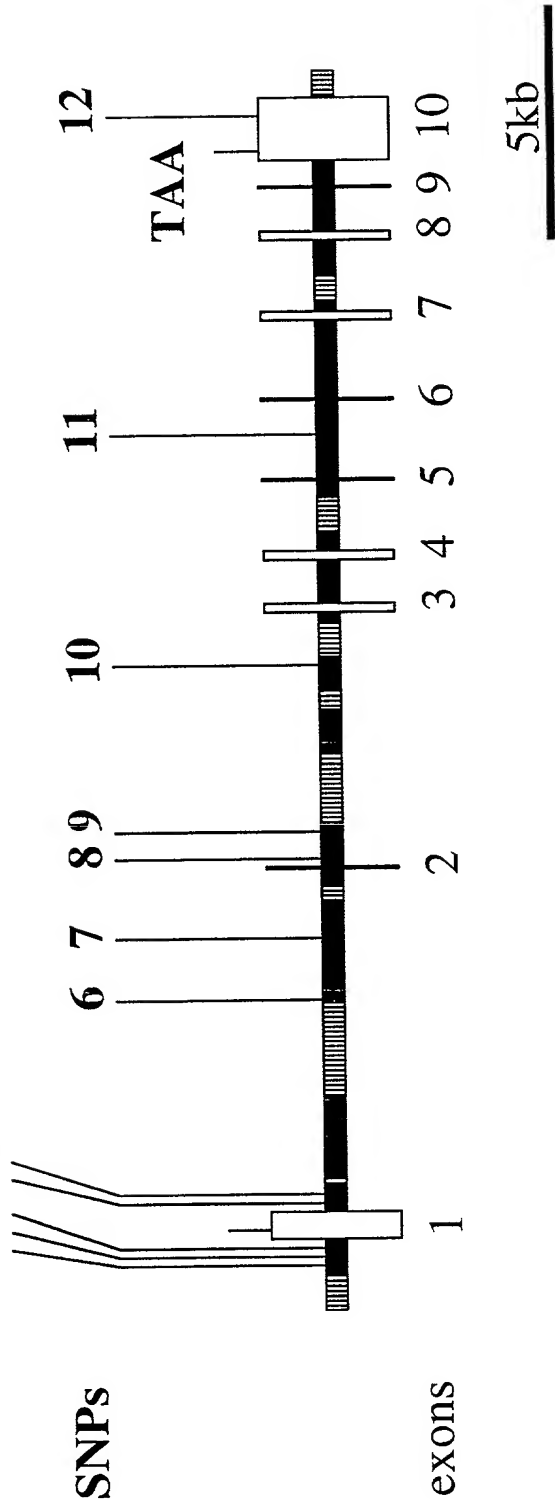


Fig. 183 Solute carrier family 22 (organic cation transporter), member 1
(SLC22A1, OCT1)

ACCESSION AL35625.5

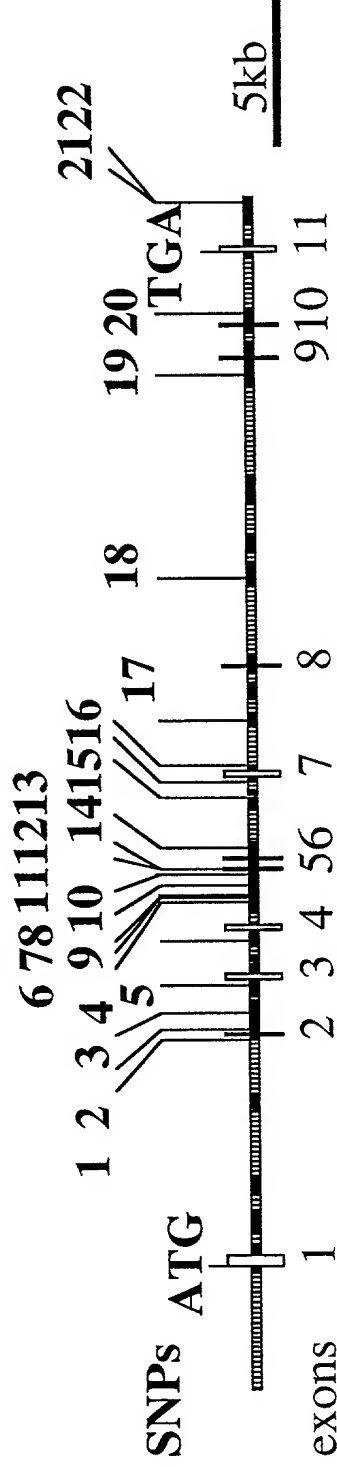


Fig. 184 Solute carrier family 22 (organic cation transporter), member 2
(SLC22A2, OCT2)

ACCESSION AL162582.18

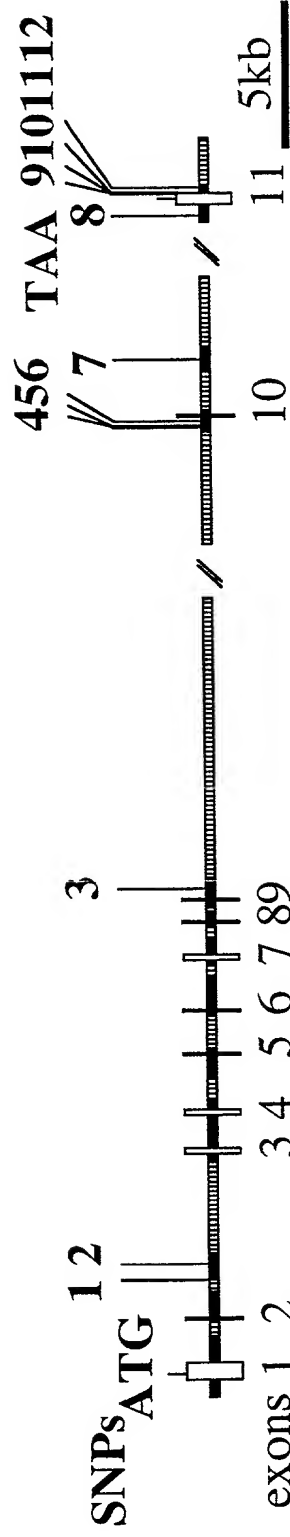


Fig. 185

Solute carrier family 10, member 2 (SLC10A1)²
Na/taurocholate cotransporting polypeptide (NTCP)

ACCESSION AL157789.6

TAG

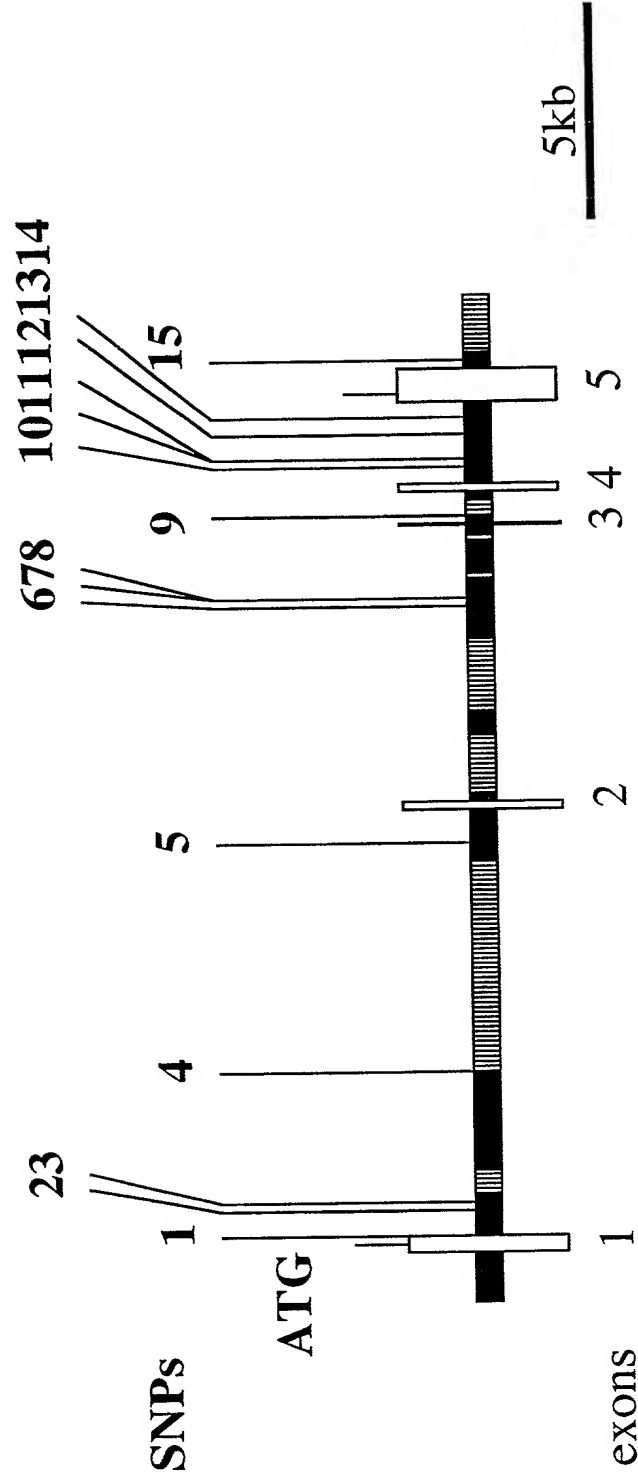


Fig. 186

Solute carrier family 15, member 1 (SLC15A1)
Oligopeptide transporter, member 1 (PEPT1)

ACCESSION AL353574.8 AL391670.6

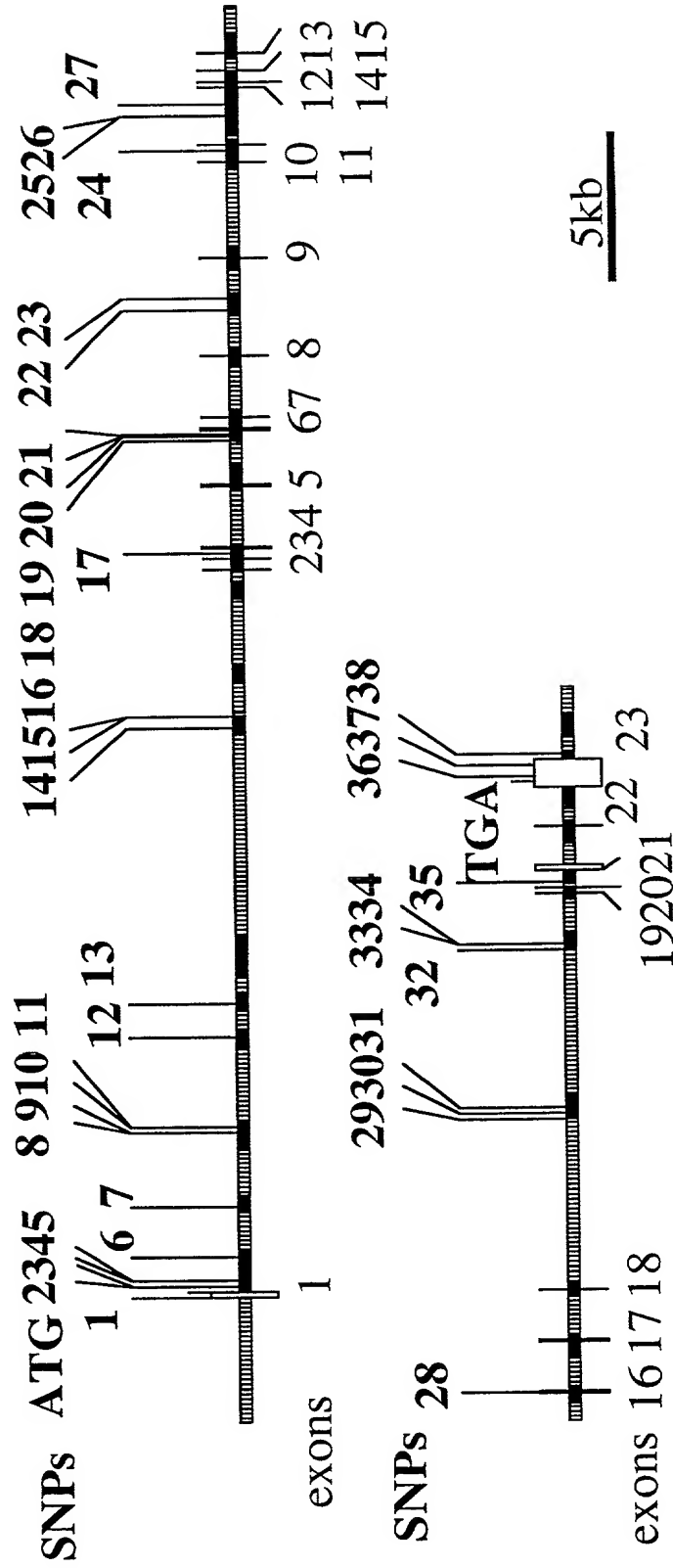


Fig. 187

Epoxide hydrolase 1, microsomal (EPHX1)

ACCESSION AC058782.8

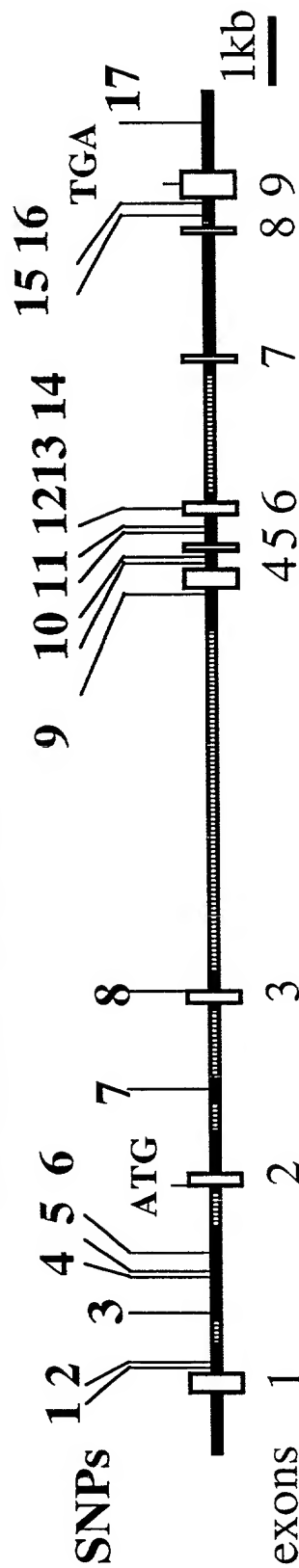


Fig. 188

Epoxide hydrolase, cytoplasmic (EPHX2)

ACCESSION AC010856.3

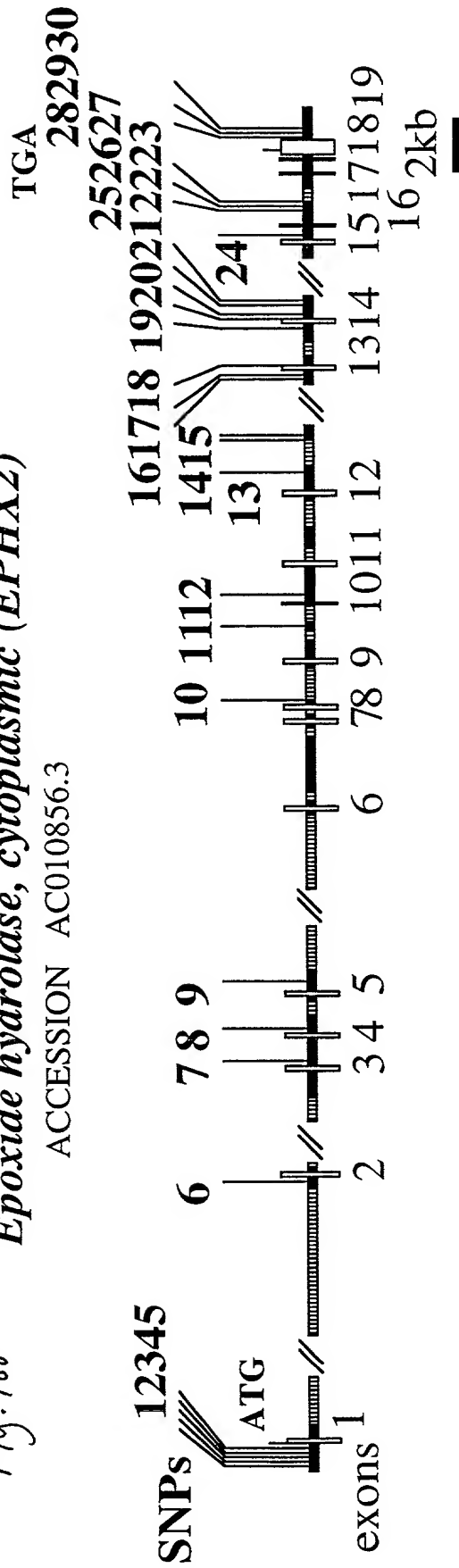


Fig. 189

Catechol-O-methyltransferase (COMT)

ACCESSION AC000080.2

141516

ATG111213

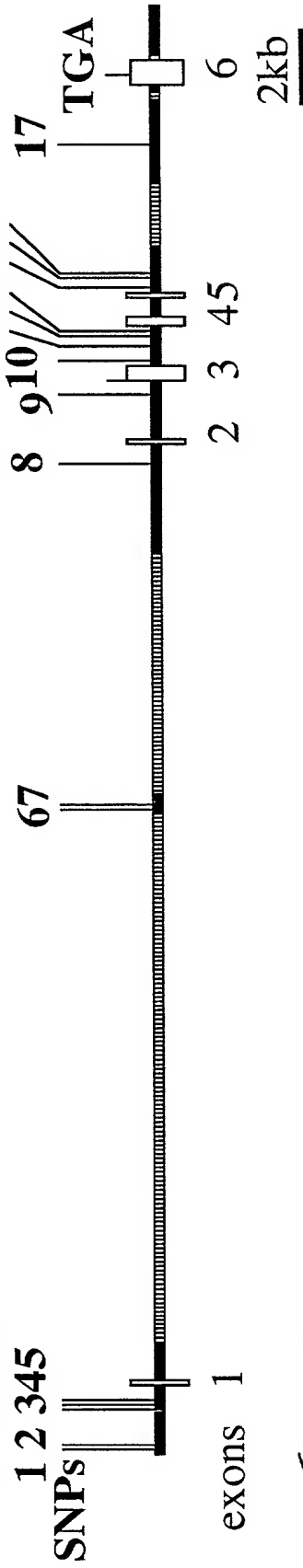


Fig. 190

Guanidinoacetate N-methyltransferase (GAMT)

ACCESSION NT_000879.1

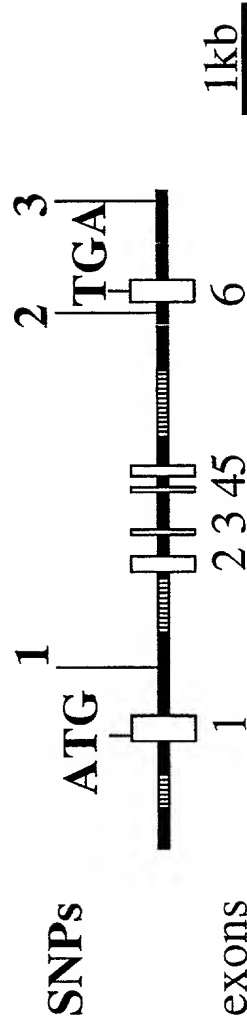


Fig. 191 *Phenylethanolamine N-methyltransferase*

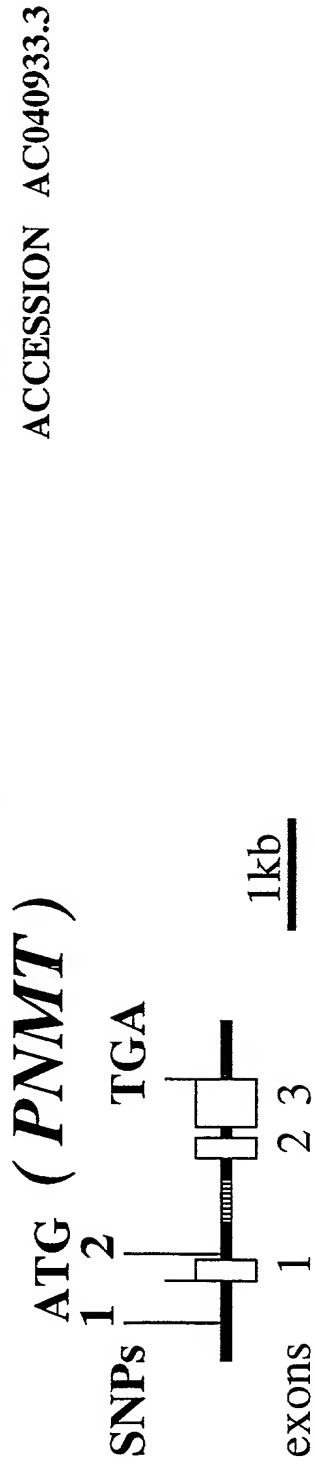


Fig. 192 *Histamine N-methyltransferase (HNMT)*

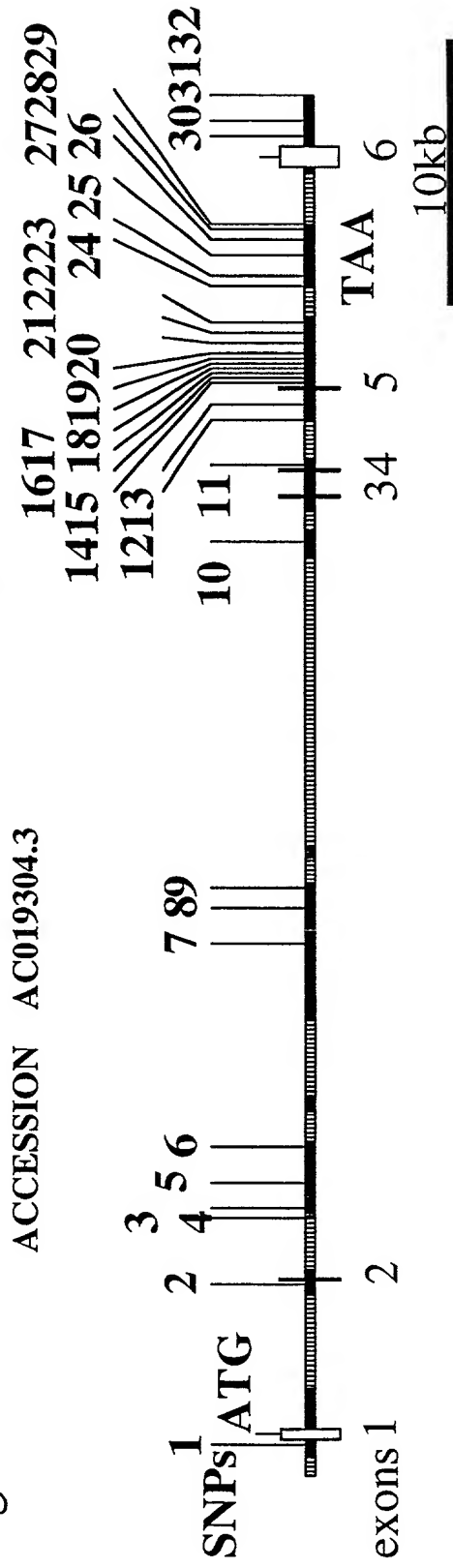


Fig. 193 Nicotinamide N-methyltransferase (NNMT)

ACCESSION AC019290.3

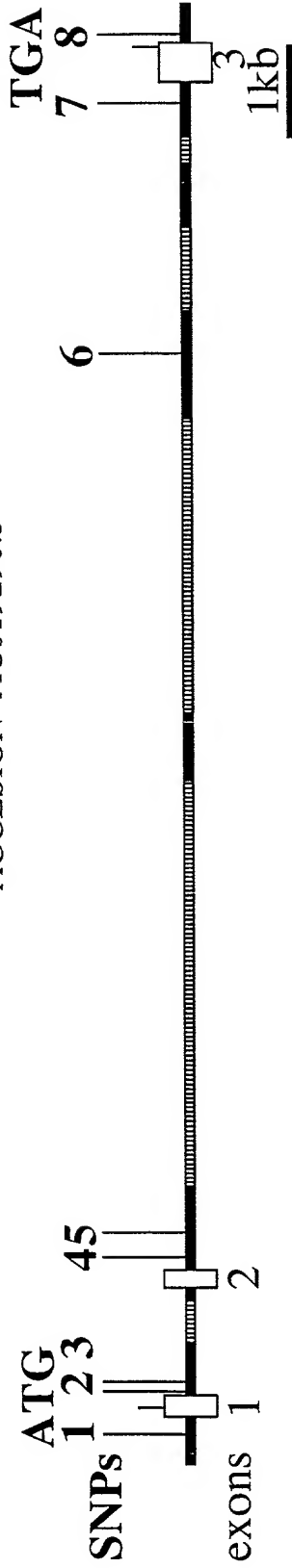


Fig. 194 Phosphatidylethanolamine N-methyltransferase (PEMT)

ACCESSION AC020558.3

TGA

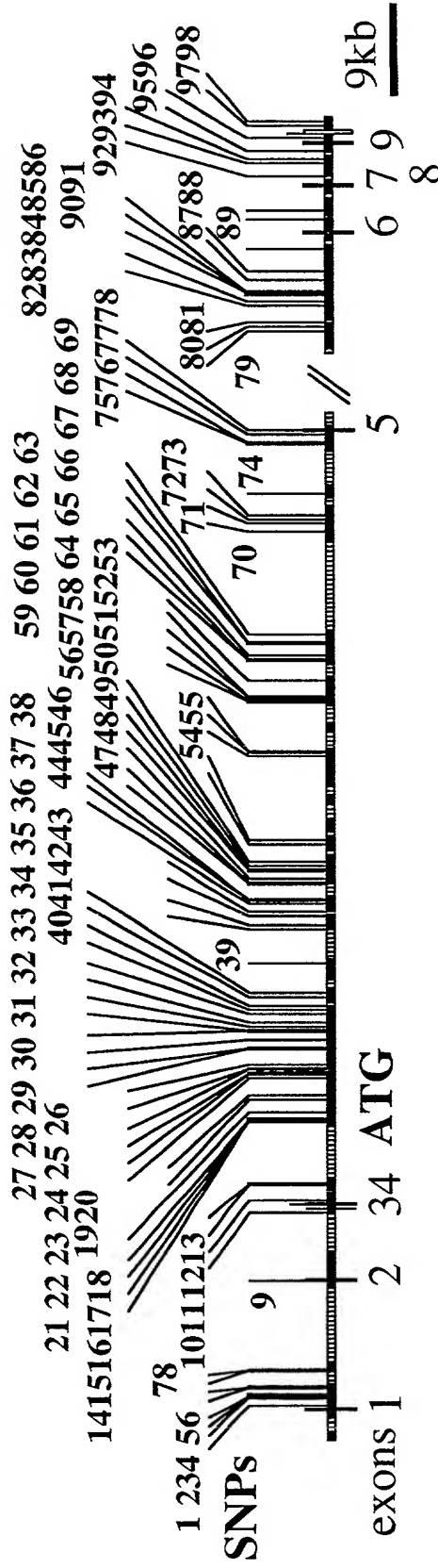


Fig. 195

*Aldehyde dehydrogenase 1 family,
member A1 (ALDH1A1)*

ACCESSION AC009284.2
AL162416.3

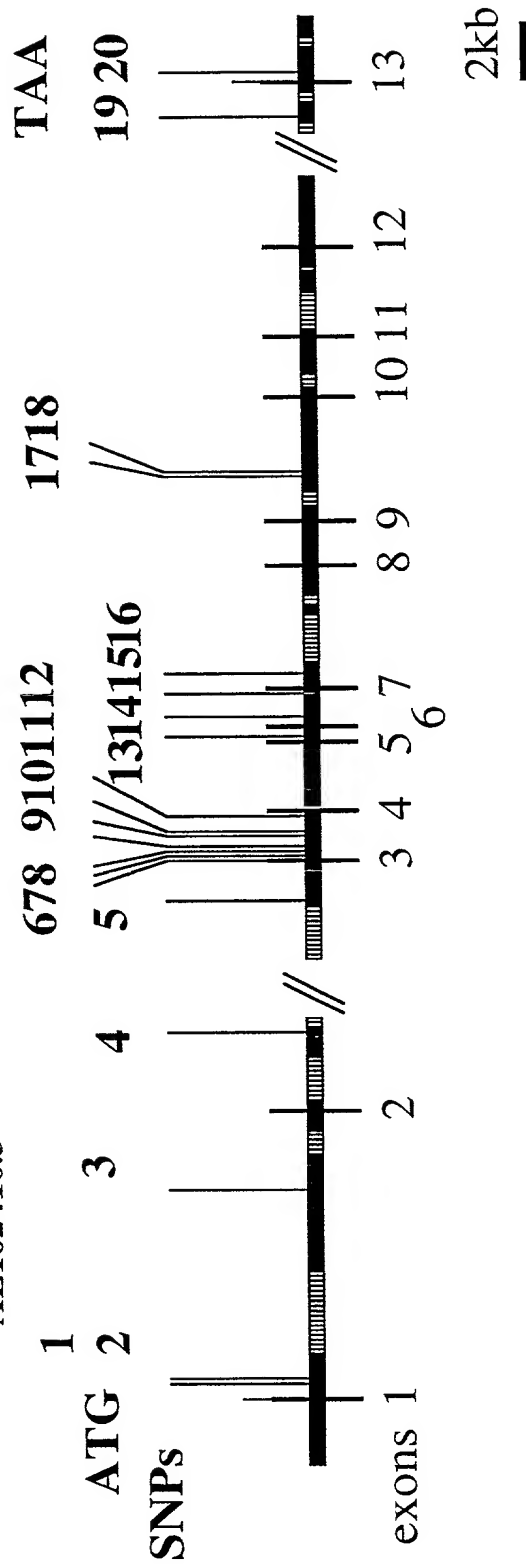


Fig. 196

Aldehyde dehydrogenase 1 family, member A2 (ALDH1A2)

ACCESSION AC025431.7

AC012653.8

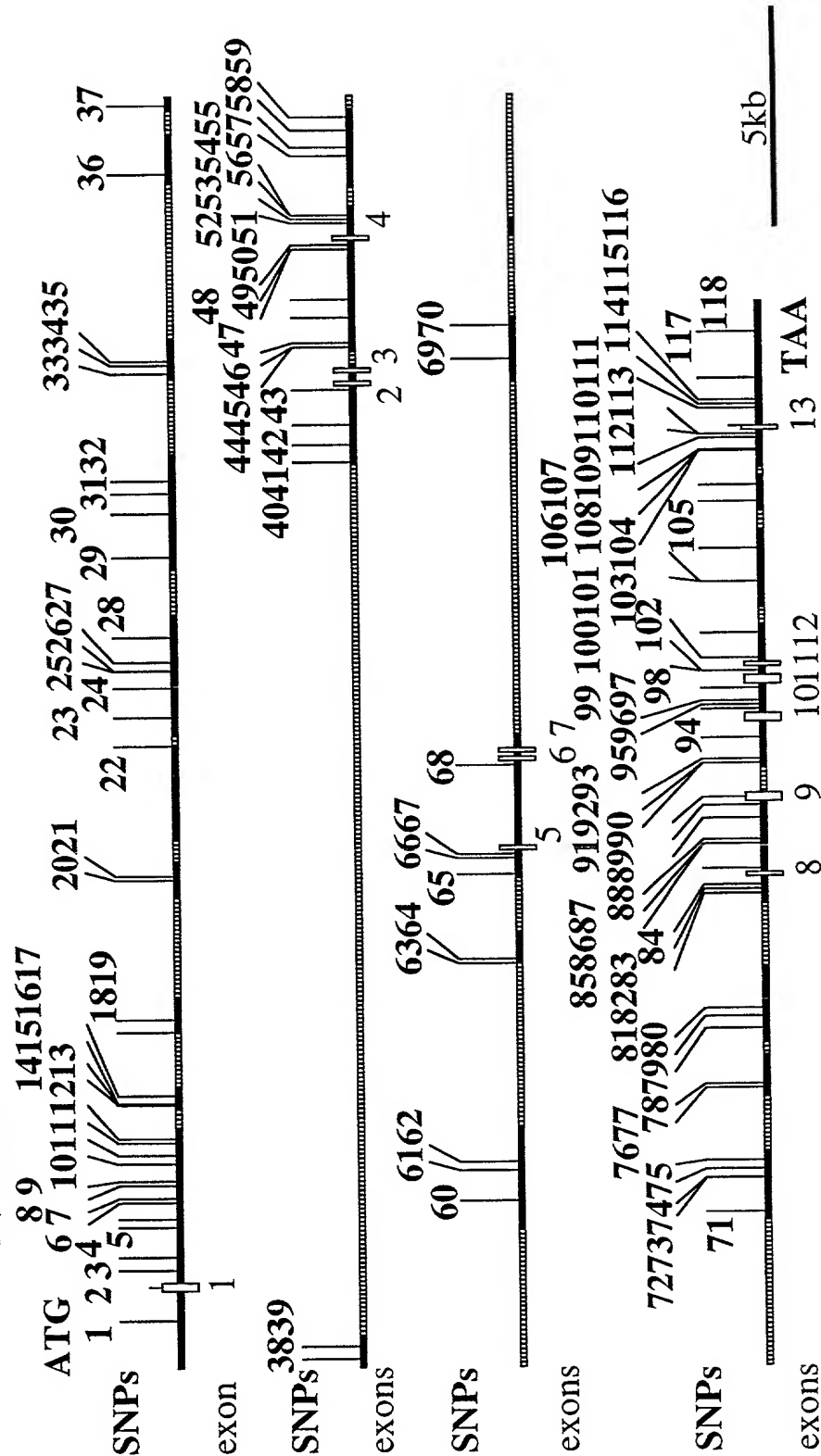


Fig. 197 *Aldehyde dehydrogenase 1 family, member A3 (ALDH1A3)*

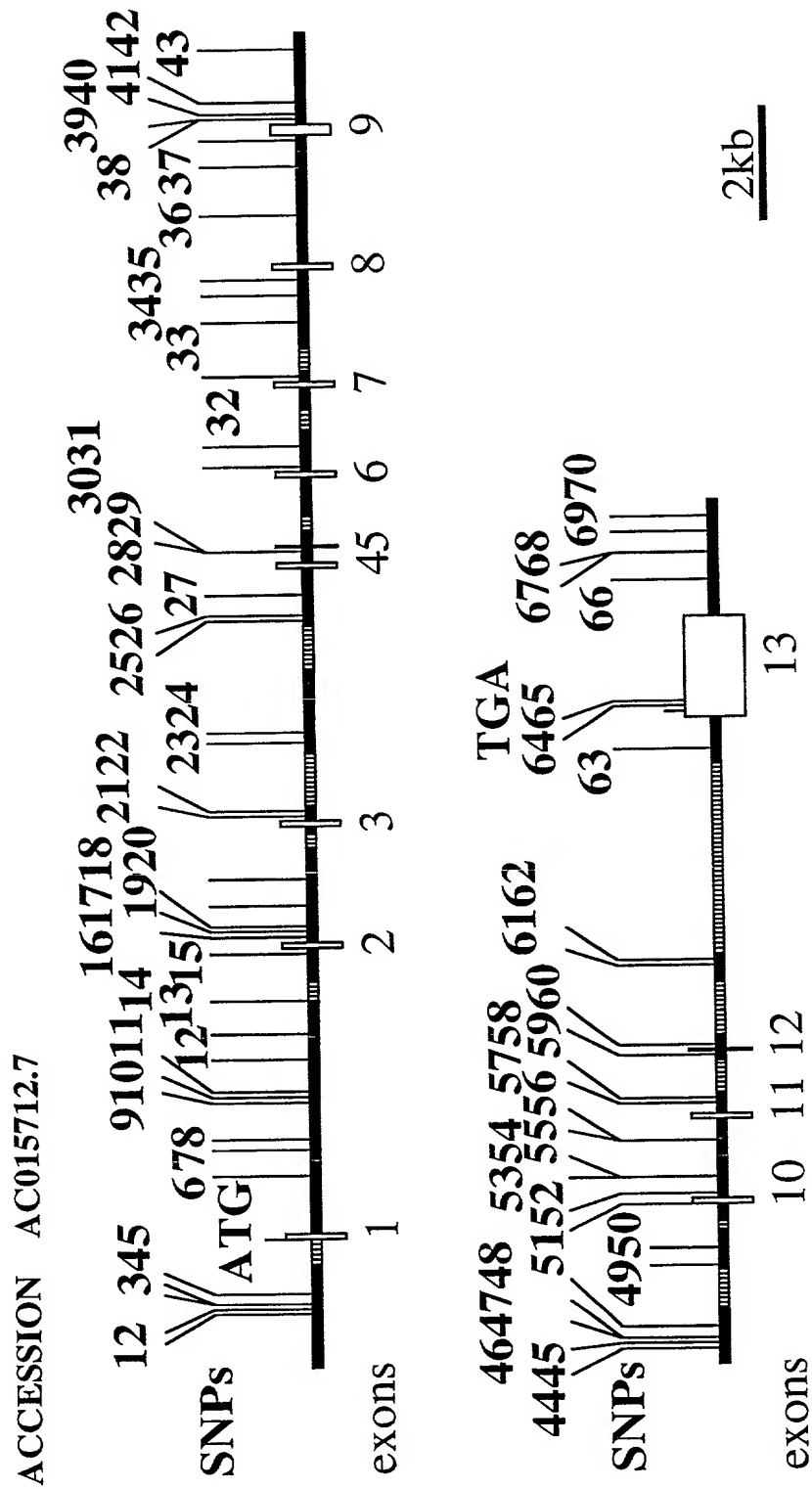


Fig. 198
Aldehyde dehydrogenase 1 family, member B1 (ALDH1B1)

ACCESSION AL135785.9

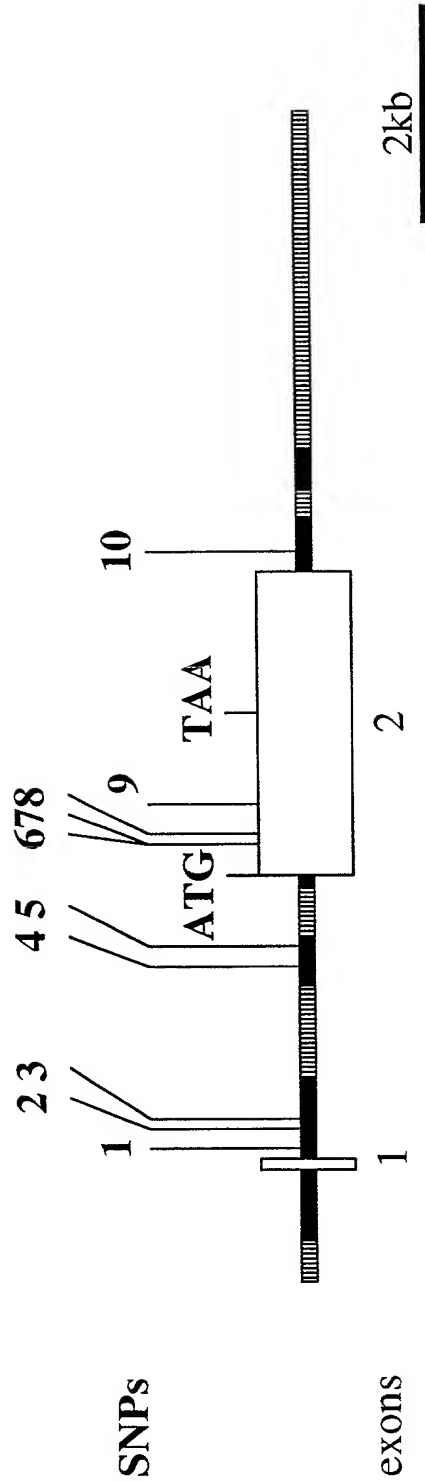


Fig. 199A *Formyltetrahydrofolate dehydrogenase (FTHFD)*
Aldehyde dehydrogenase 1 family, member L1 (ALDH1L1)

ACCESSION AC079848.6

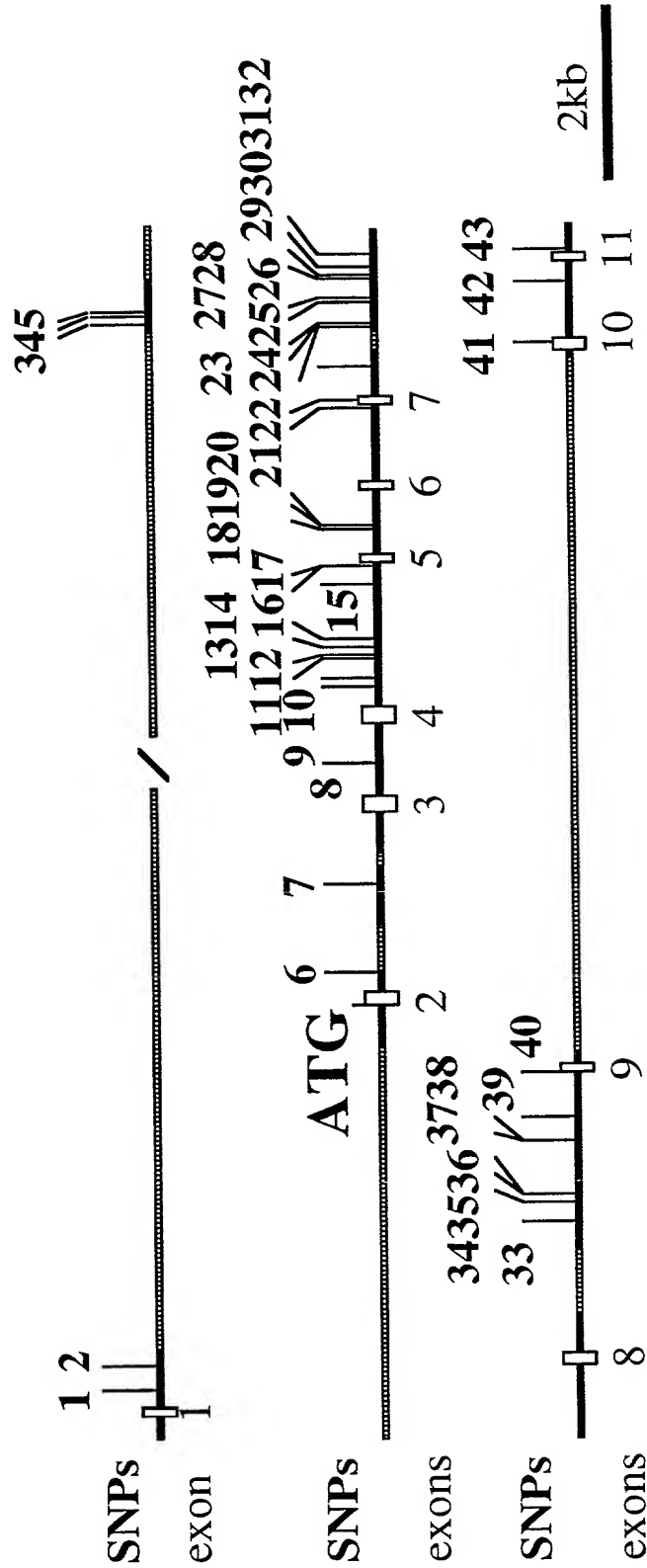


Fig. 199B

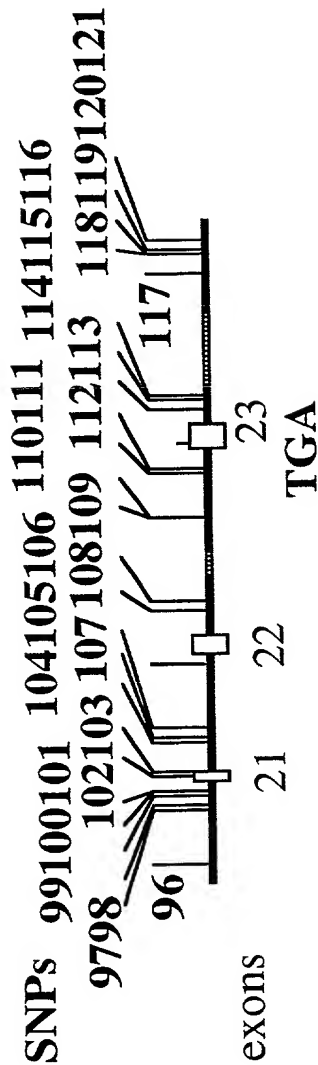
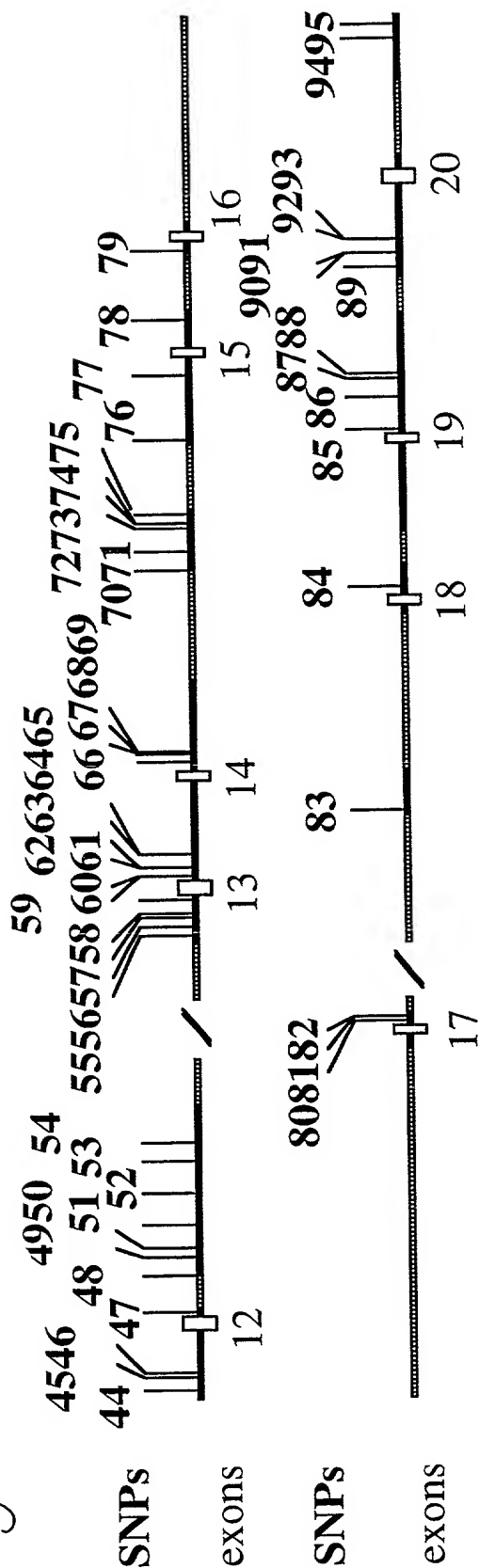


Fig. 200 Aldehyde dehydrogenase 2 (ALDH2)

ACCESSION AC002996.1
AC003029.2

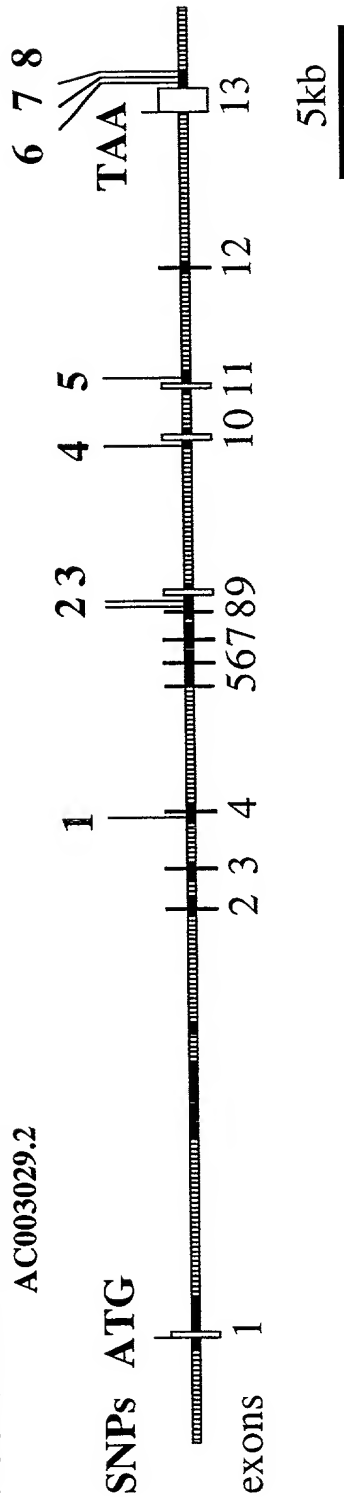


Fig. 201 Aldehyde dehydrogenase 3 family, member A1 (ALDH3A1)

ACCESSION AC005722.1

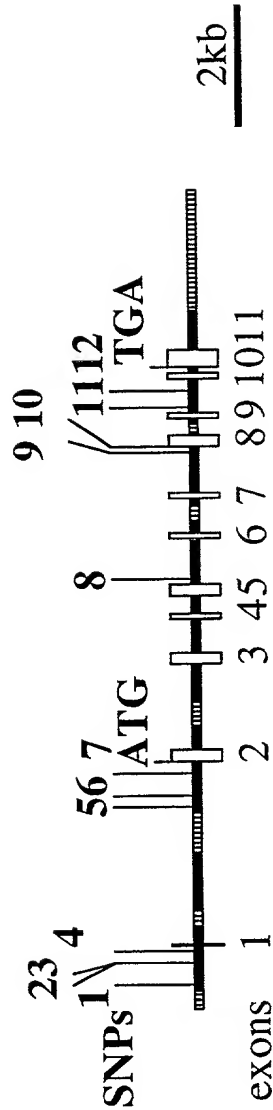


Fig. 202 Aldehyde dehydrogenase 3 family, member A2
(ALDH3A2)
ACCESSION AC005722.1

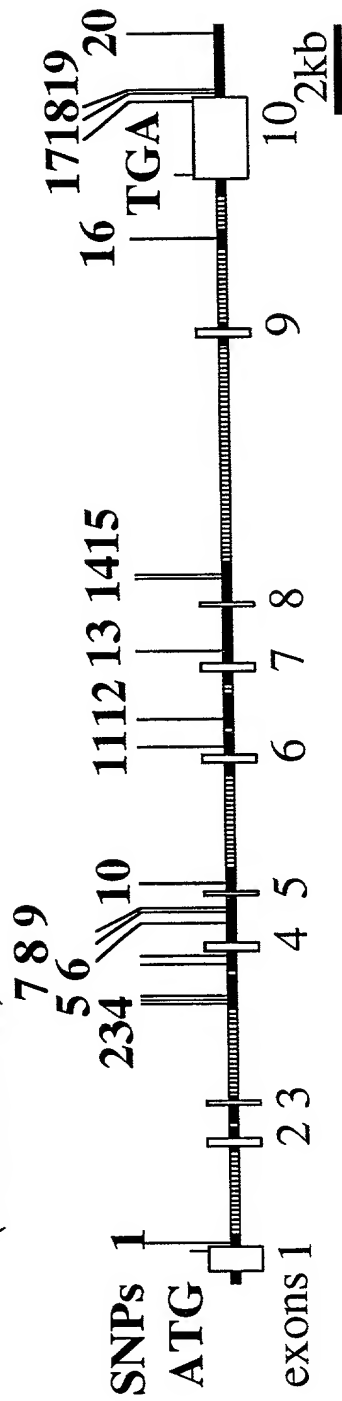


Fig. 203 Aldehyde dehydrogenase 3 family, member B1 (ALDH3B1)
ACCESSION AC004923.2

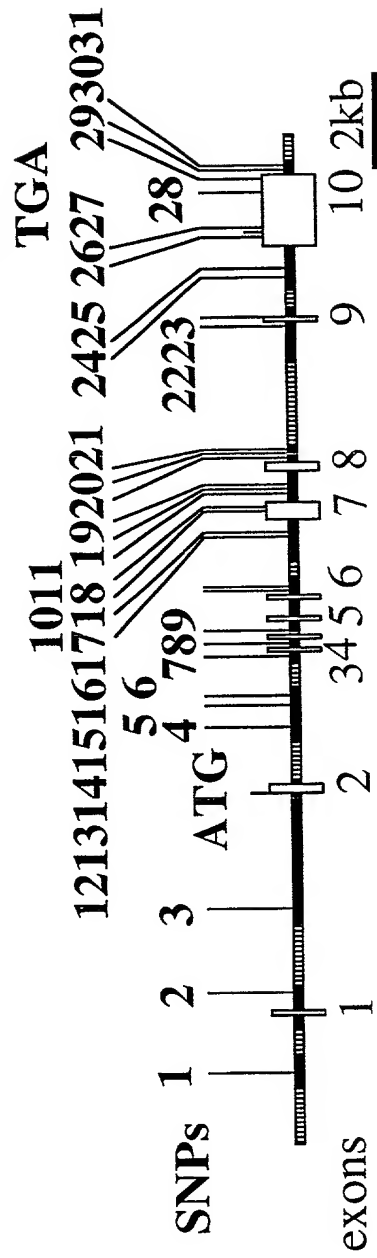


Fig. 204 Aldehyde dehydrogenase 3 family, member B2 (ALDH3B2)

ACCESSION AC021987.3

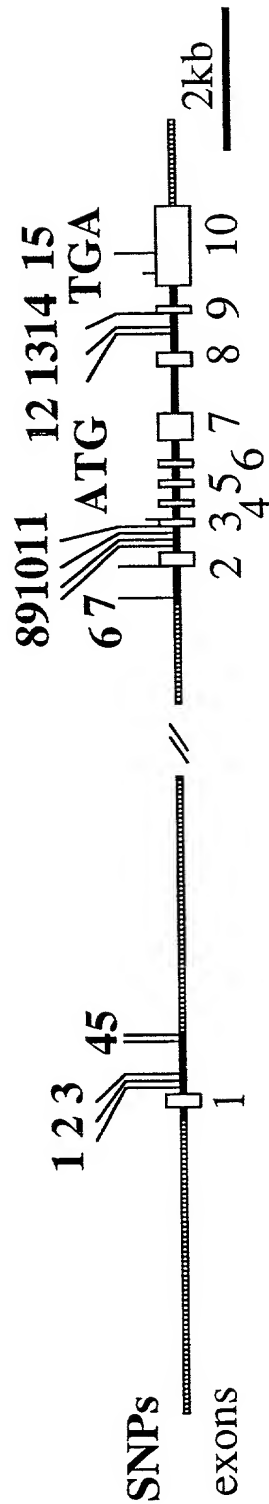


Fig. 205 Aldehyde dehydrogenase 5 family, member A1 (ALDH5A1)

ACCESSION AL031230.1

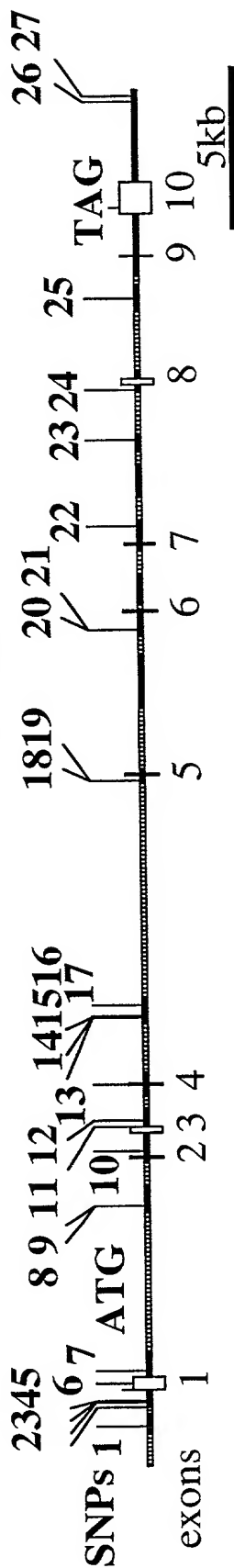


Fig. 206 Aldehyde dehydrogenase 6 family, member A1 (ALDH6A1)

ACCESSION AC005484.2

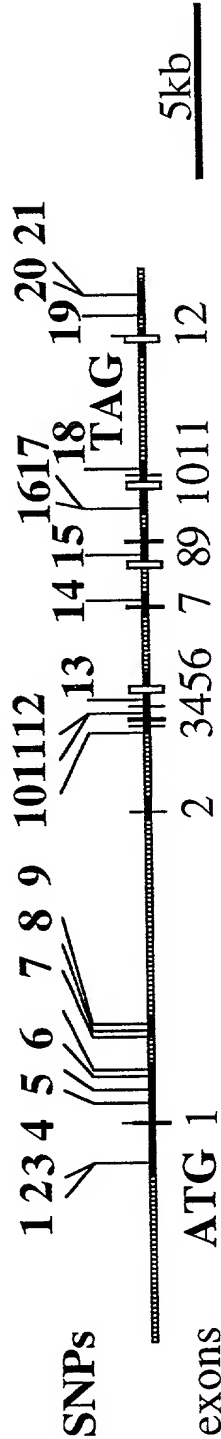


Fig. 207 Aldehyde dehydrogenase 8 family,
member A1 (*ALDH8A1*)

ACCESSION AL445190.9
AL021939.1

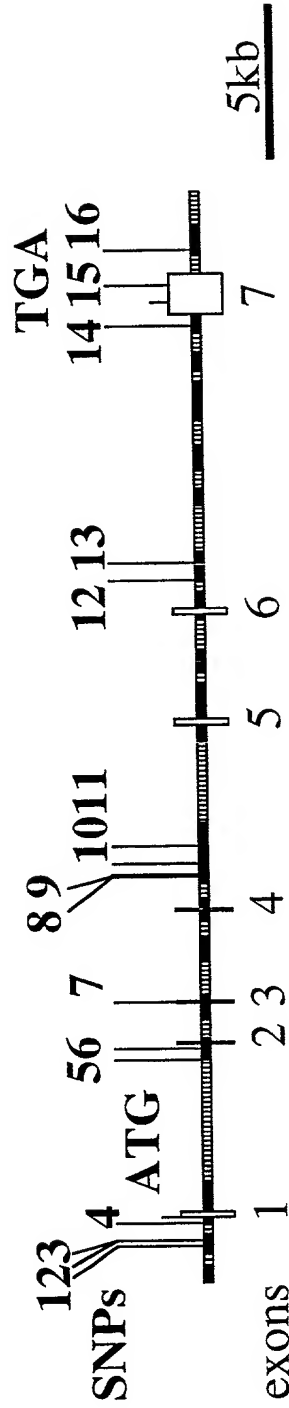


Fig. 208 Aldehyde dehydrogenase 9 family,
member A1 (*ALDH9A1*)

ACCESSION AL451074.4

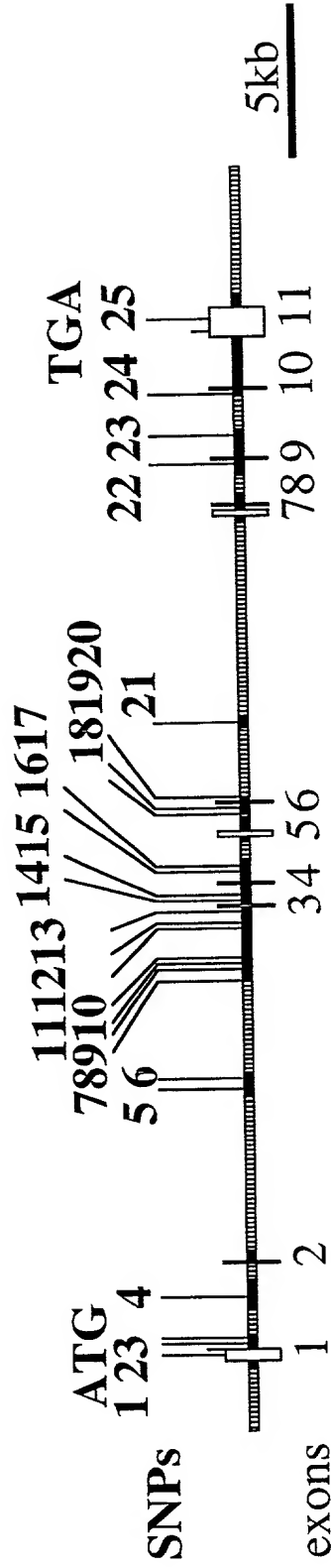


Fig. 209 Alcohol dehydrogenase 1 (*ADH1*)

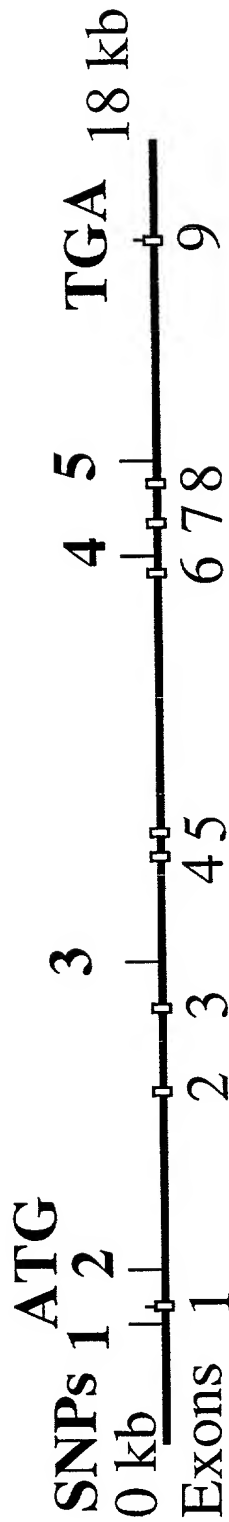


Fig. 210 Alcohol dehydrogenase 2 (*ADH2*)

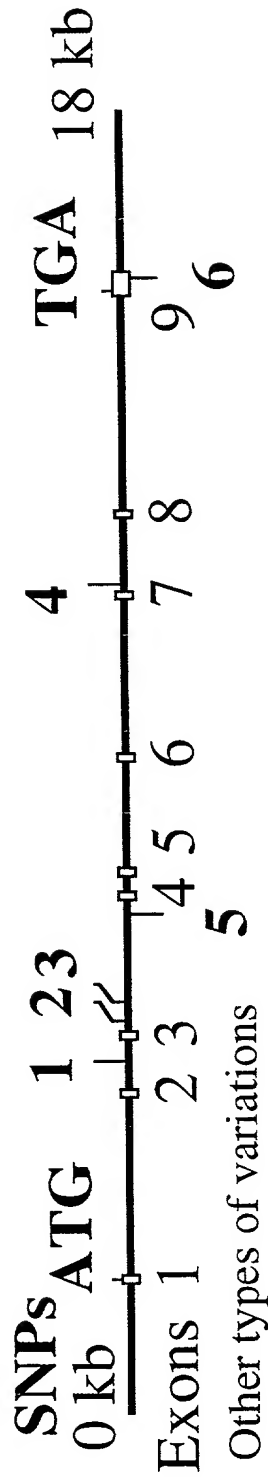


Fig. 211 Alcohol dehydrogenase 3 (*ADH3*)

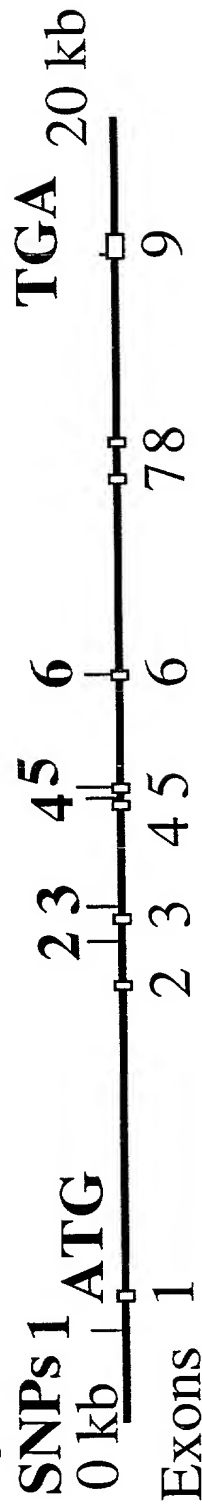
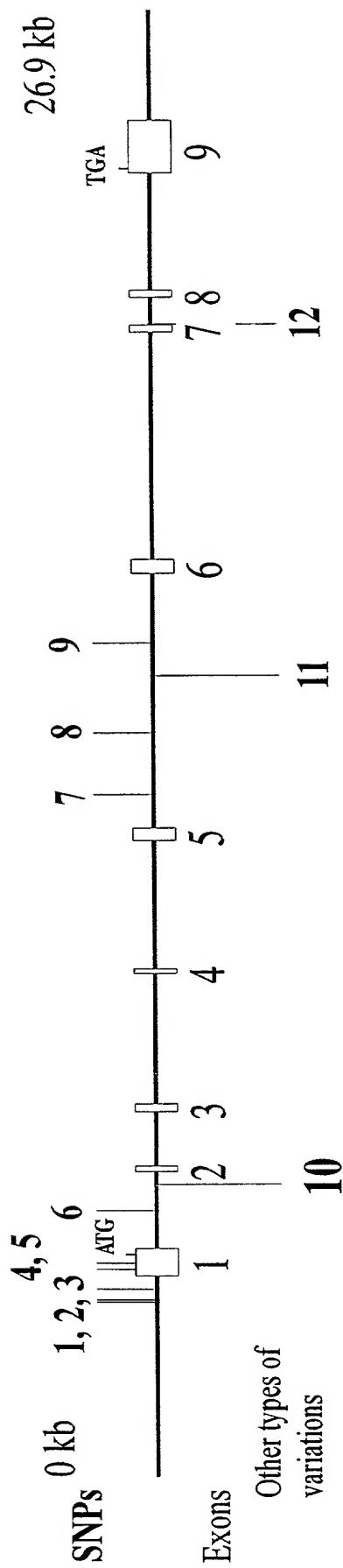


Fig. 212

Alcohol dehydrogenase 4 (*ADH4*)



NT_026300.1

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AGCCTCAGTT TCTCTTTGGT GTTCCCGCCC ACAGTTCCCG CTGTACTGGT TCAGCGTGCC
 Observed : A/G
 3' Assay : GCCATCCTGA AGGGCTGGAT GGATAGGGTG CTGTGCCAGG GCTTTGCCTT TGACATCCCA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
 Chromosome : 6
 map
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
 Position in Sequence : 171597 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_026300.1.20010416.9
 Amplified region : 171031..172143 in NT_026300
 size : 1113
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075292

12/17/2001

Fig. 216 Short-chain alcohol dehydrogenase family gene
(HEP27)

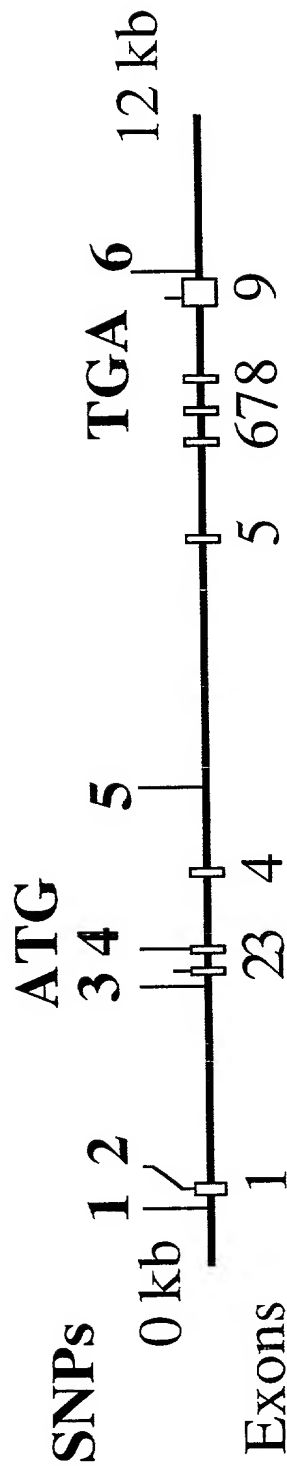


Fig. 2/17

UDP glycosyltransferase 1 family, peptide A1
(*UGT1A1*)

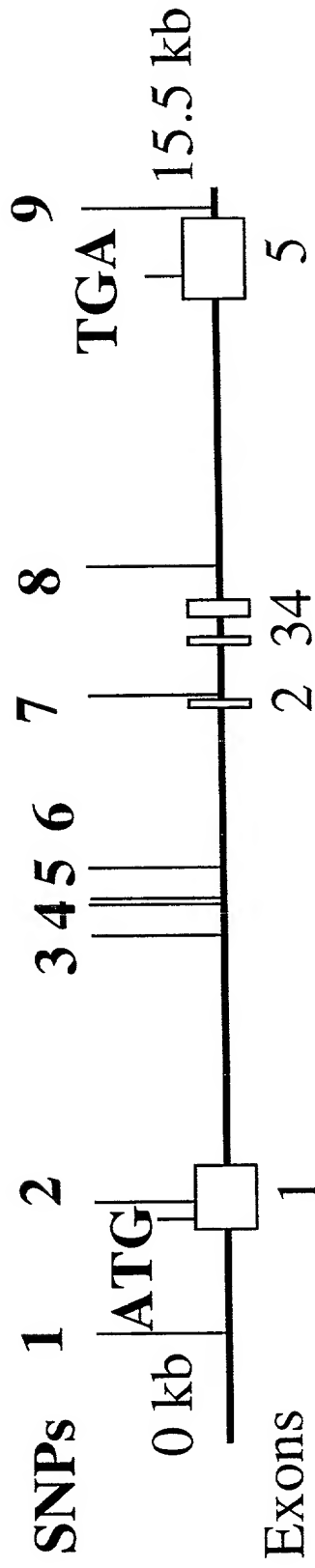


Fig. 218

UDP glycosyltransferase 2 family, polypeptide A1 (UGT2A1)

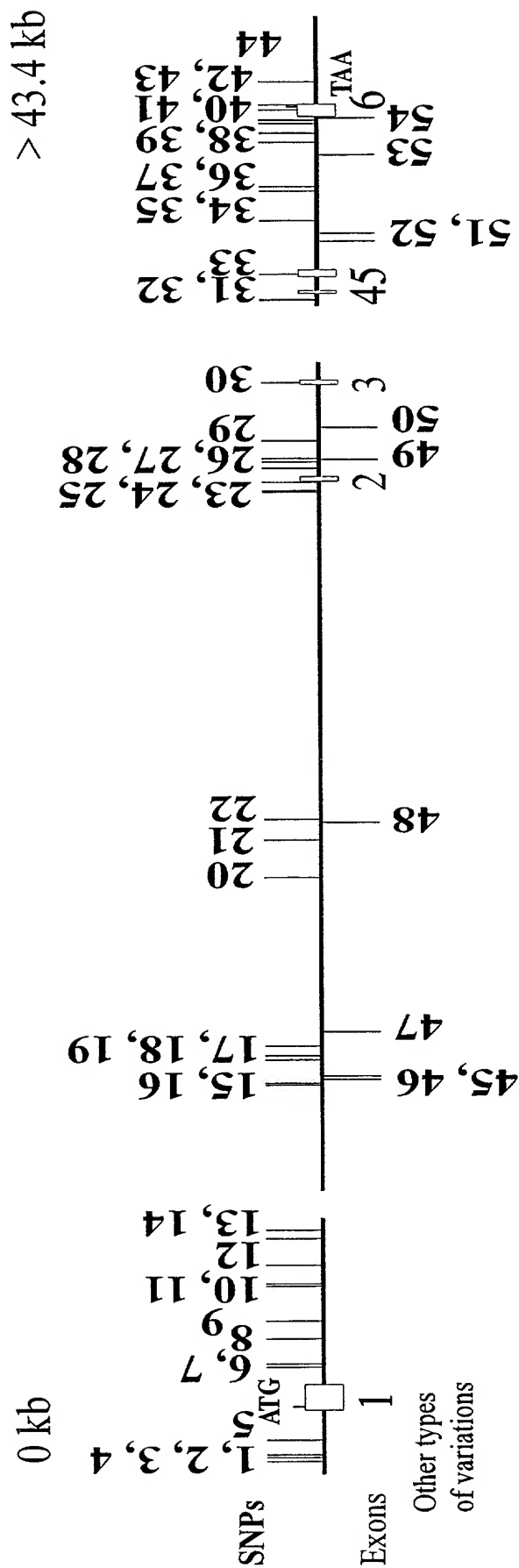


Fig. 219

UDP-glycosyltransferase 2 family, polypeptide B15(*UGT2B15*)

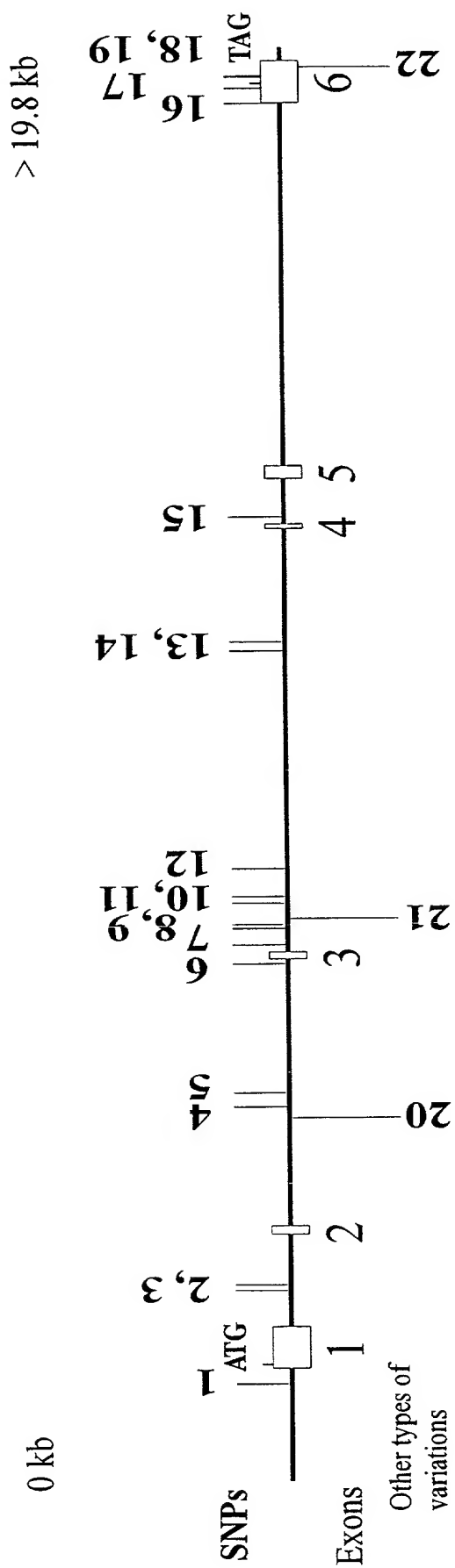


Fig. 220

UDP glycosyltransferase 8 (*UGT8*)

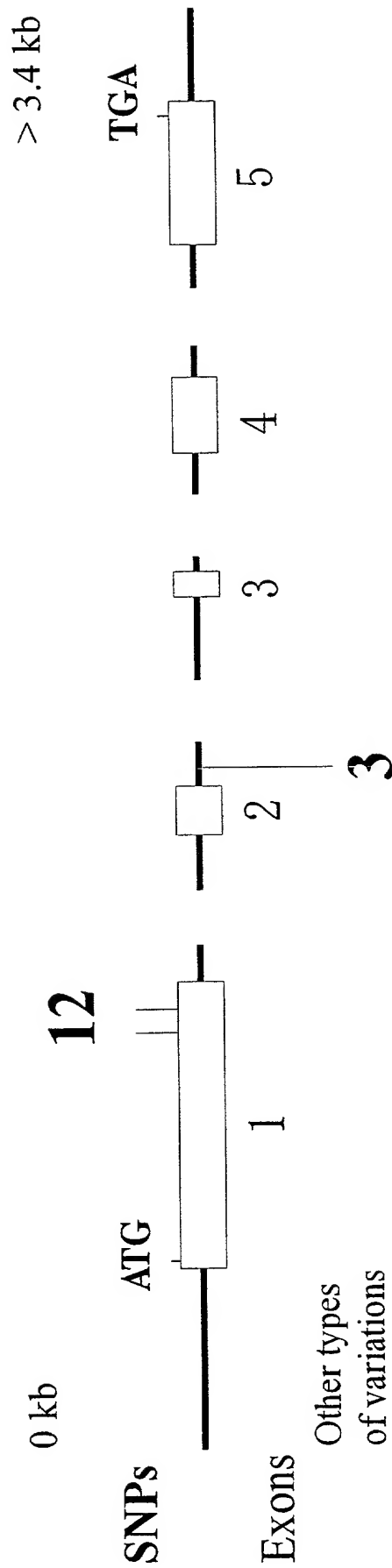


Fig. 221

Glutathione S-transferase A1 (*GSTA1*)

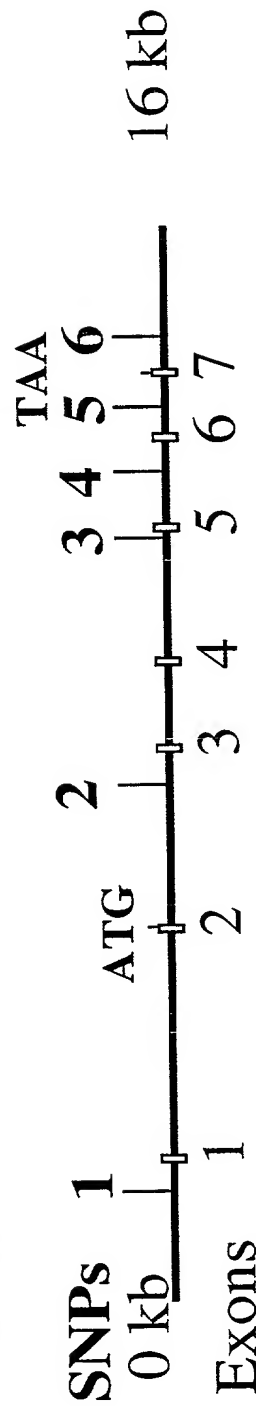


Fig. 222

Glutathione S-transferase A4 (*GSTA4*)

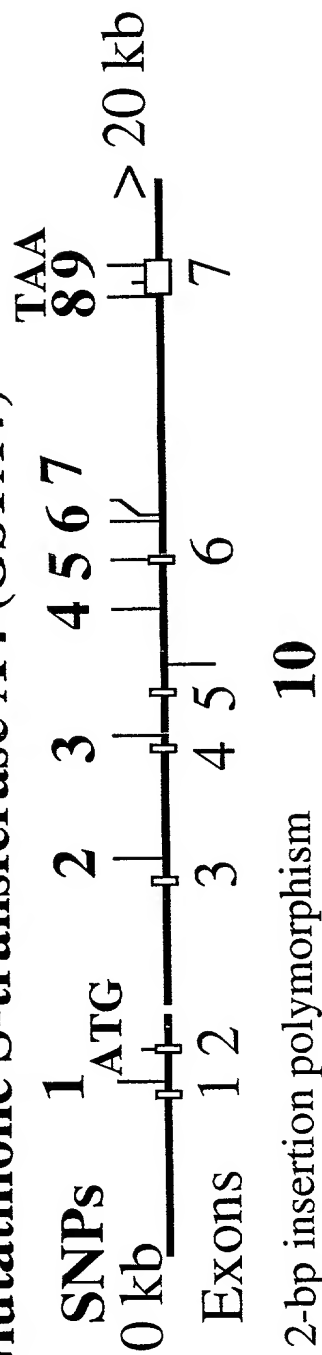


Fig. 223

Glutathione S-transferase M1 (*GSTM1*)

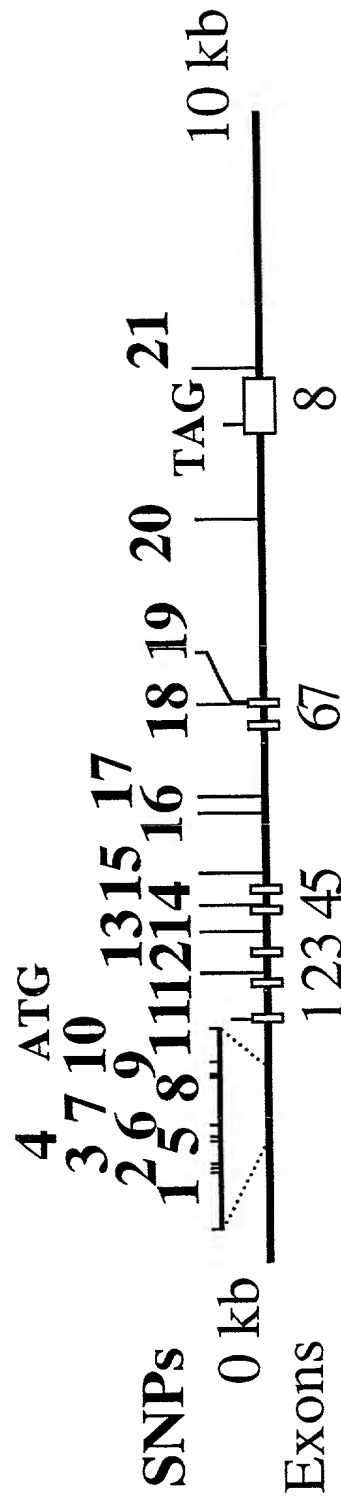


Fig. 224

Glutathione S-transferase M2 (*GSTM2*)

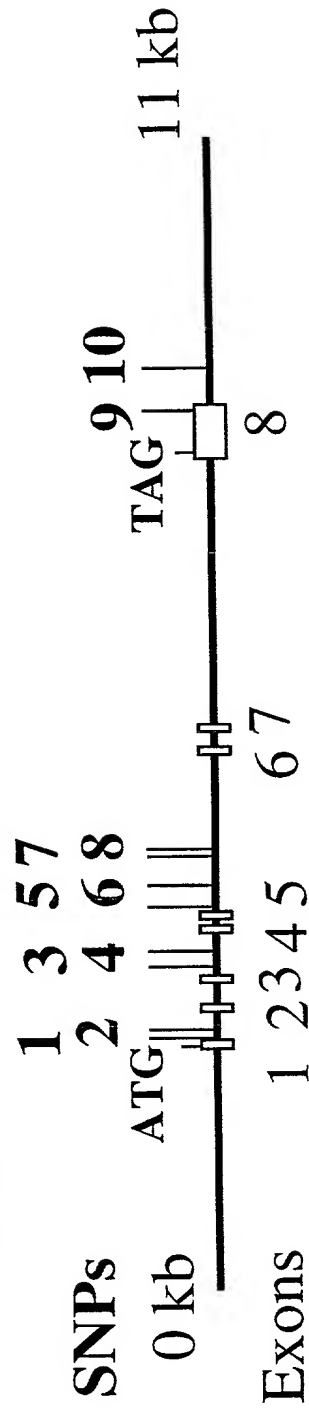


Fig. 225

Glutathione S-transferase zeta 1 (*GSTZ1*)

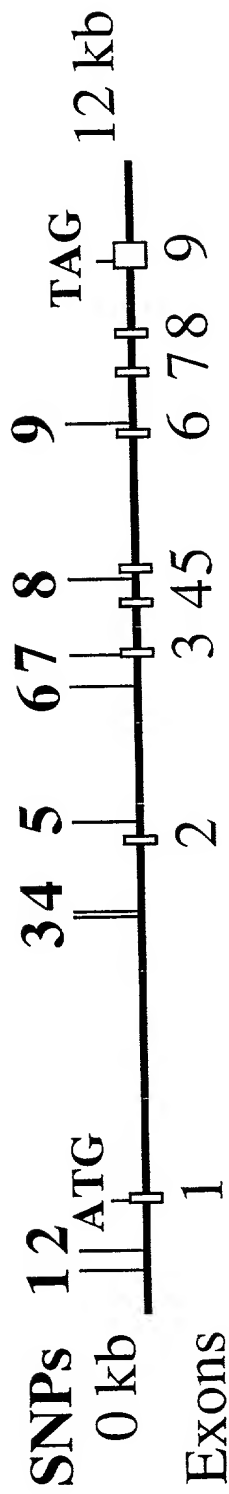


Fig. 226

Glutathione S-transferase pi (*GSTPi*)

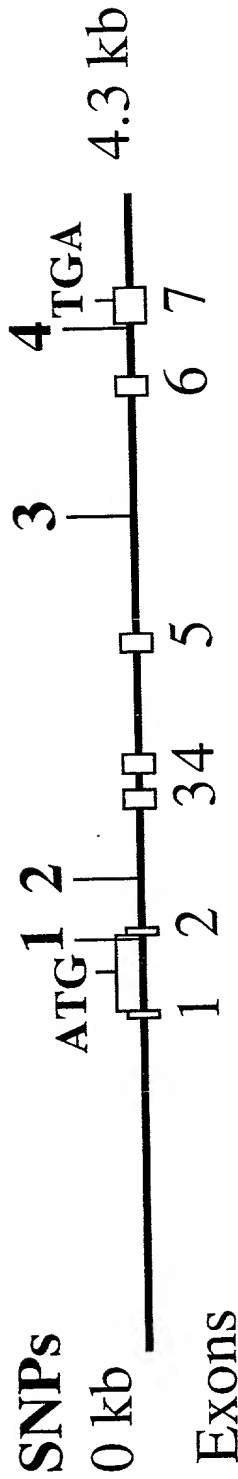


Fig. 227

Glutathione S-transferase theta 1 (*GSTT1*)

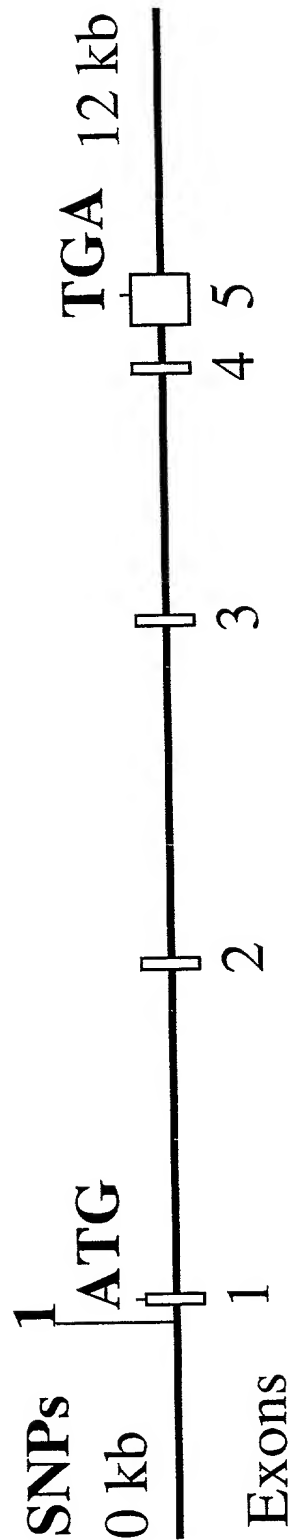


Fig. 228
Microsomal glutathione S-transferase 1 (*MGST1*)

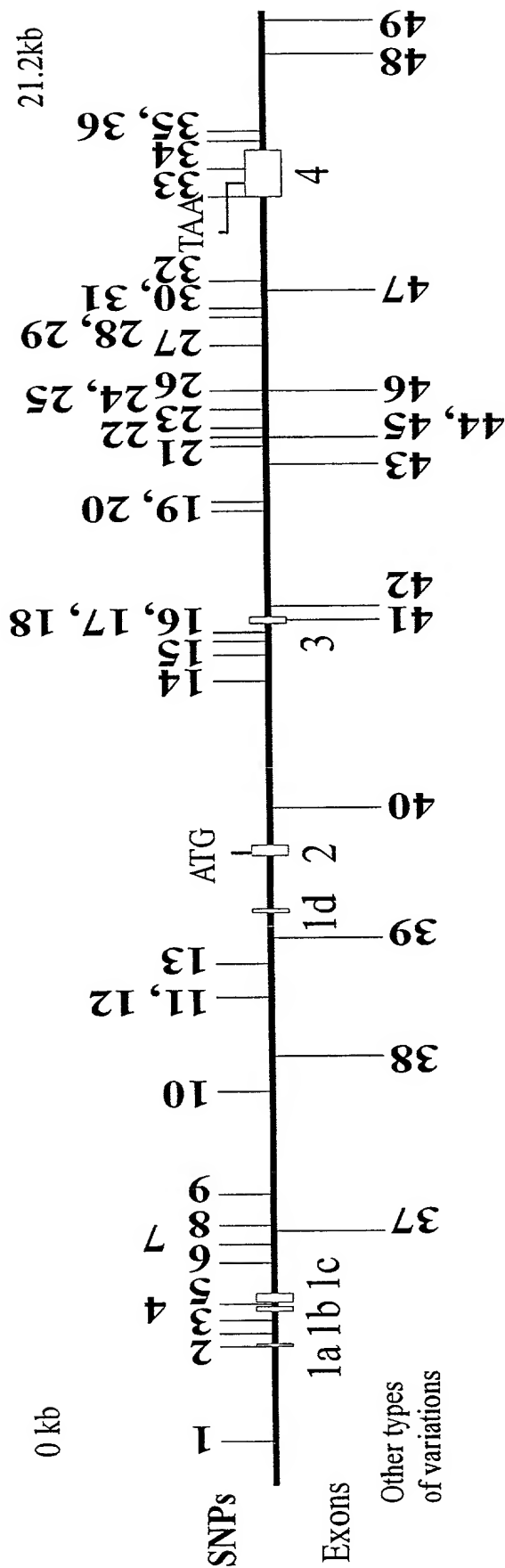


Fig. 229

Microsomal glutathione S-transferase 1-like 1 (*MGST1L1*)

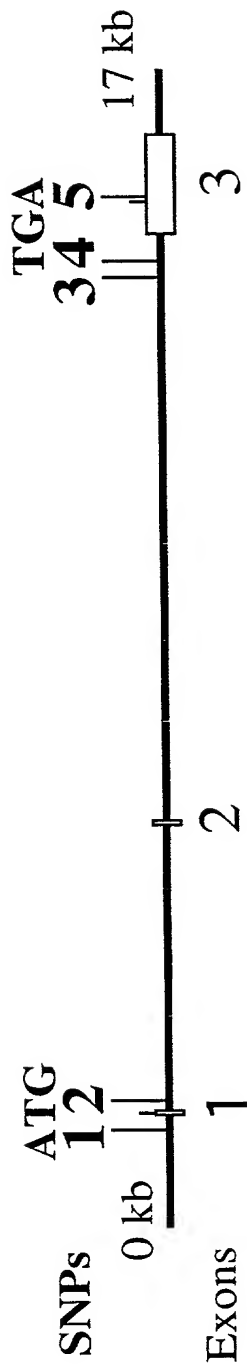


Fig. 230

Microsomal glutathione S-transferase 2 (*MGST2*): AC019049.4

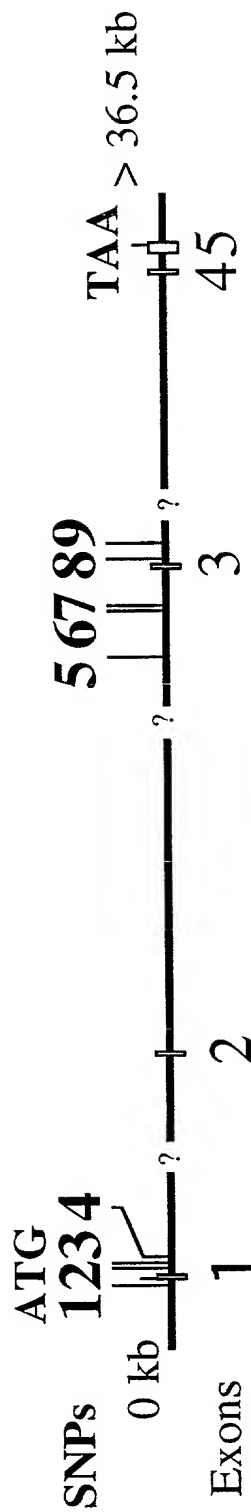


Fig. 231

Microsomal glutathione S-transferase 3 (MGST3)

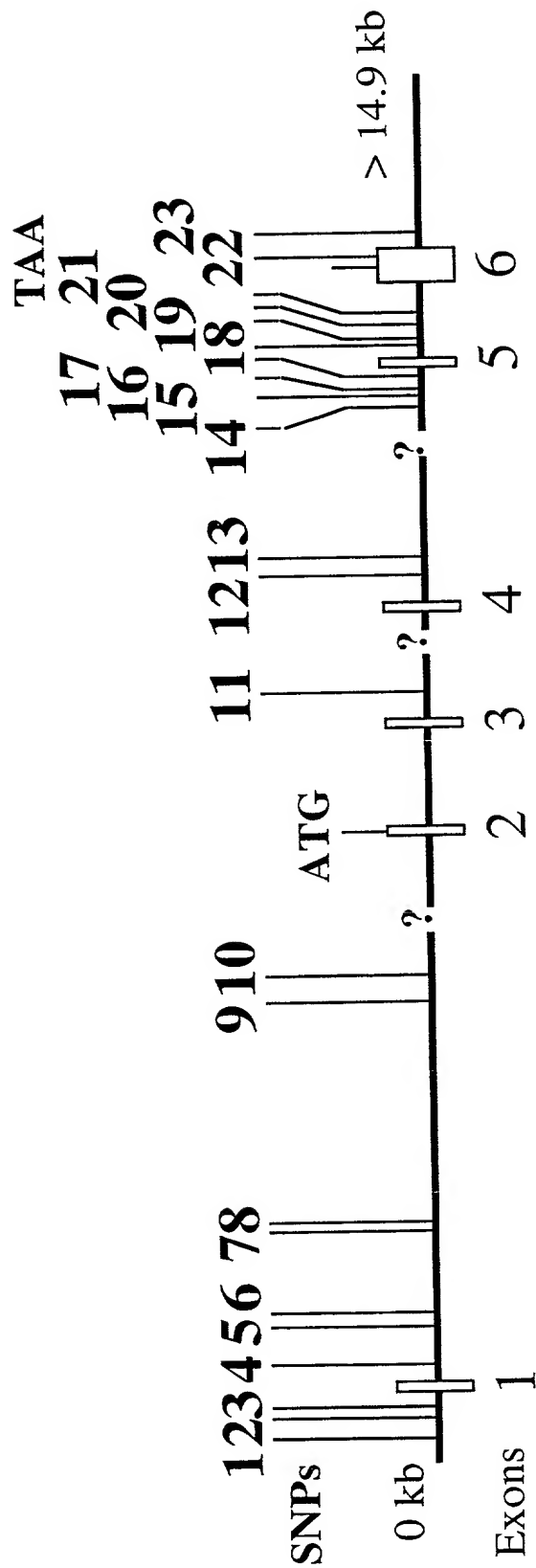


Fig. 232

Sulfotransferase 1A1 (*SULT1A1/STP1*)

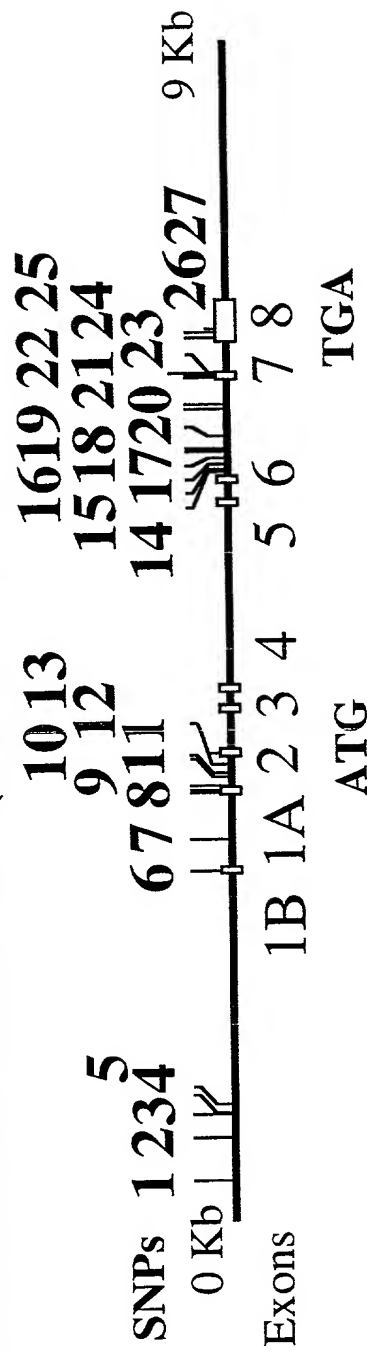


Fig. 233

Sulfotransferase 1A2 (*SULT1A2/STP2*)

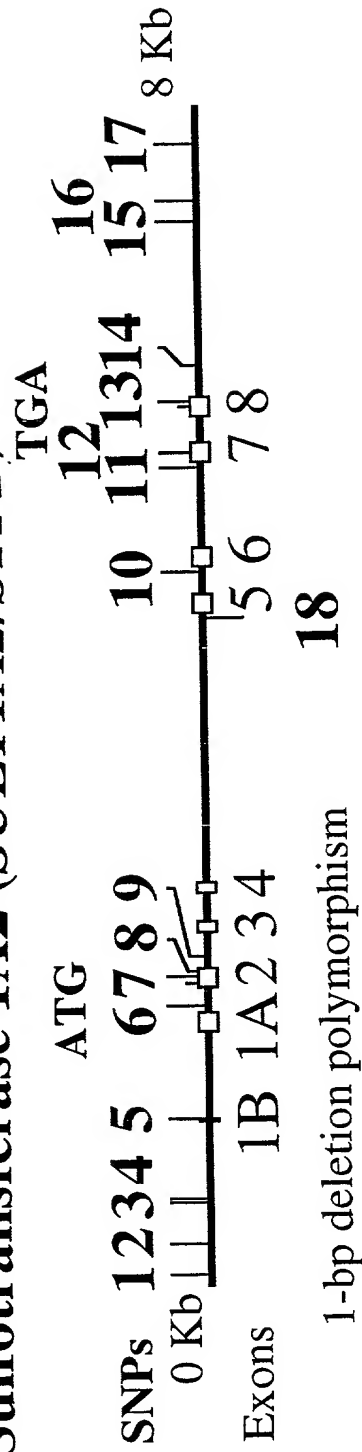


Fig. 234

Sulfotransferase 1A3 (*SULT1A3/STM/ HAST*)

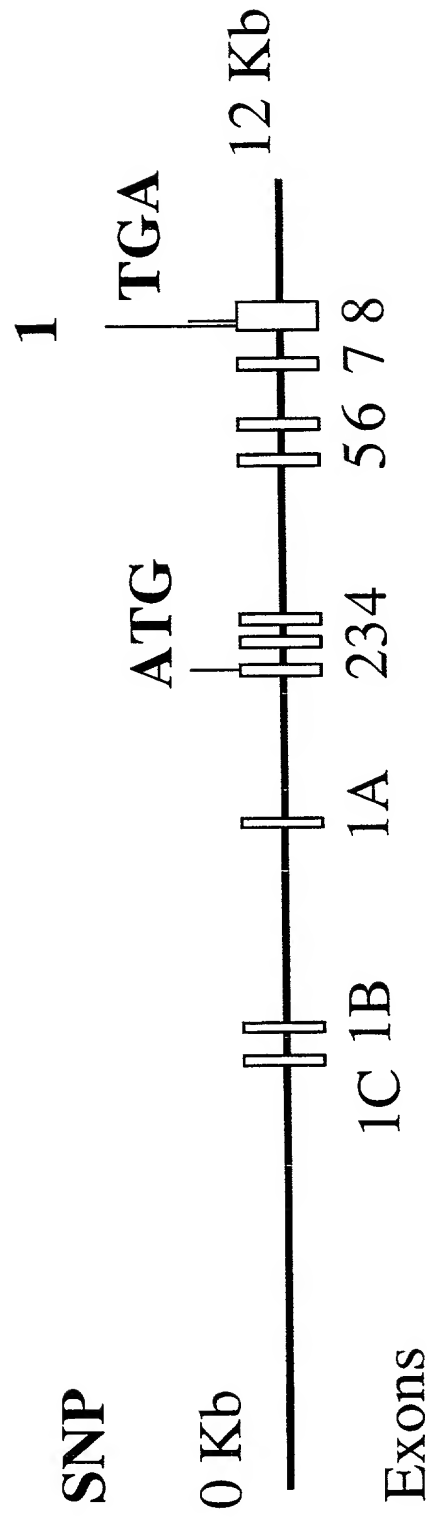


Fig. 235

Sulfotransferase 1C1 (*SULT1C1*)

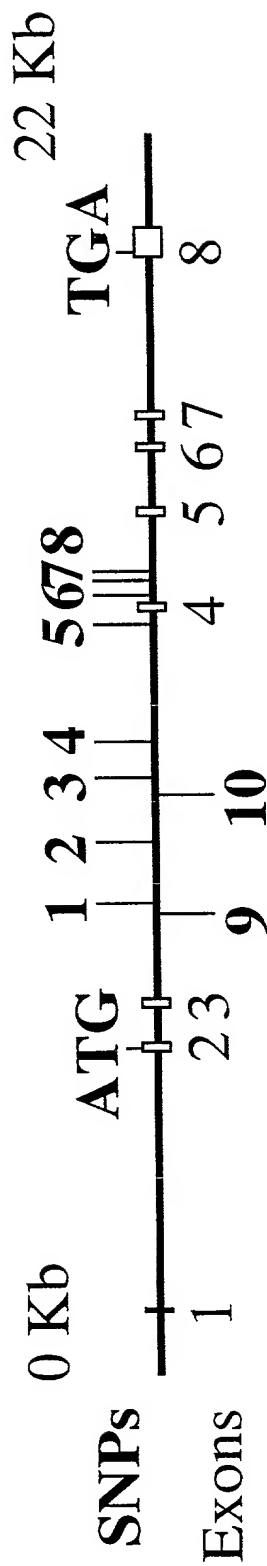


Fig. 236

Sulfotransferase 1C2 (*SULT1C2*)

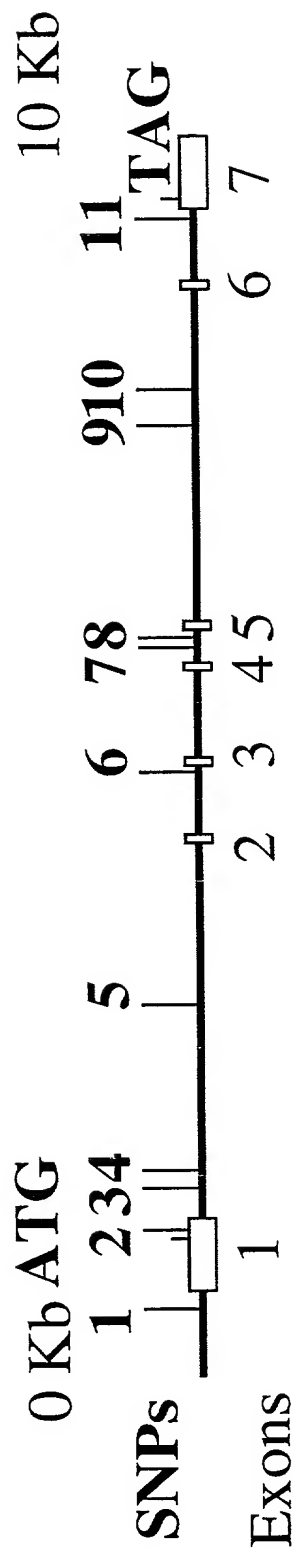


Fig. 237

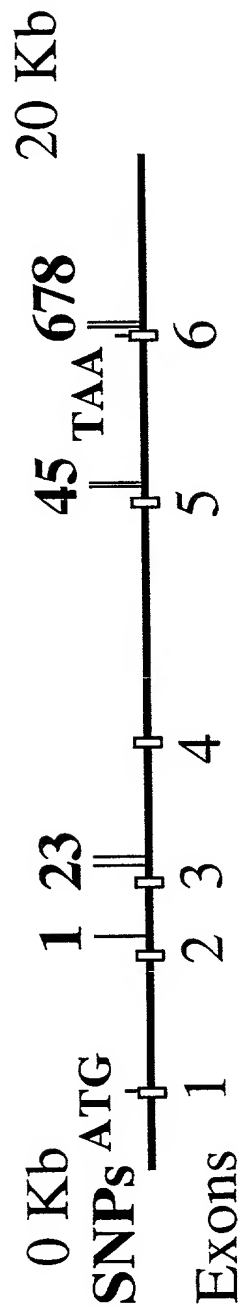


Fig. 238

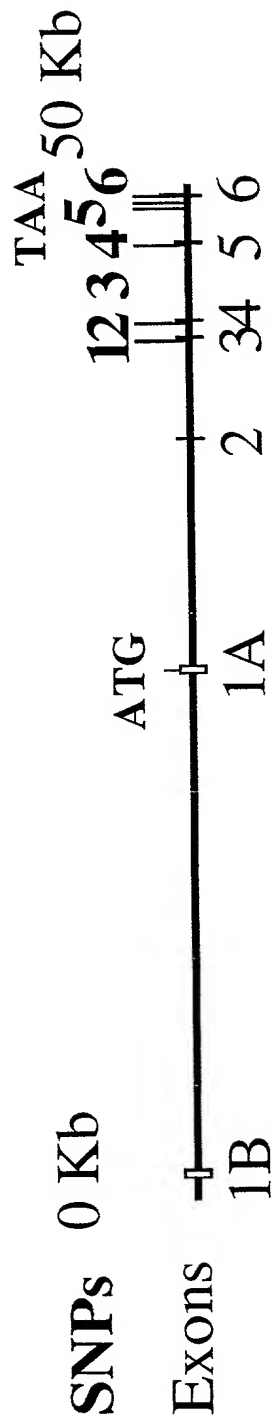


Fig. 239

Sulfotransferase-related protein 3 (*SULTX3*)

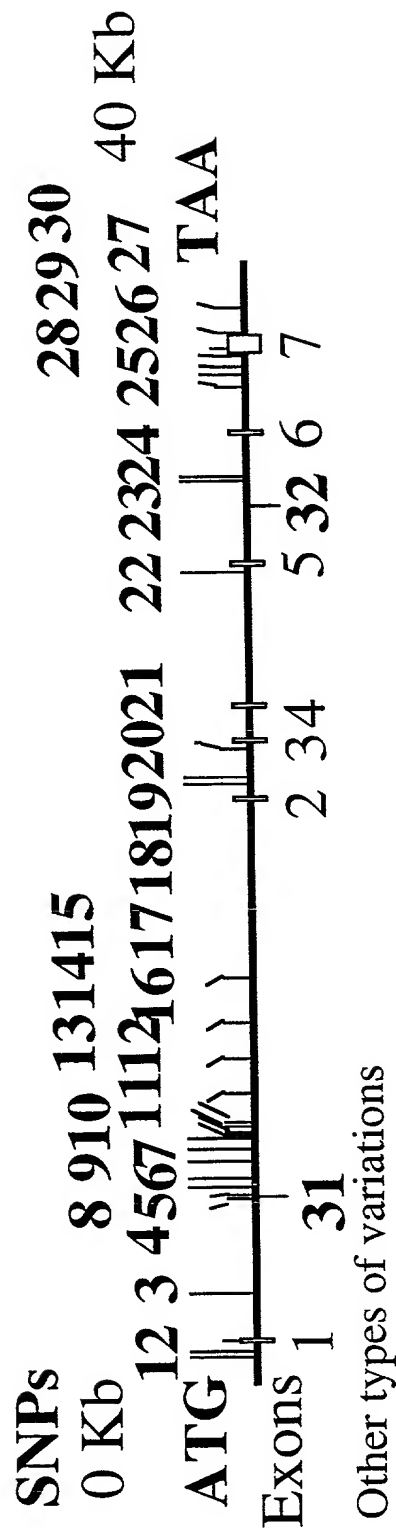


Fig. 240 Tyrosylprotein sulfotransferase 1 (*TPST1*)

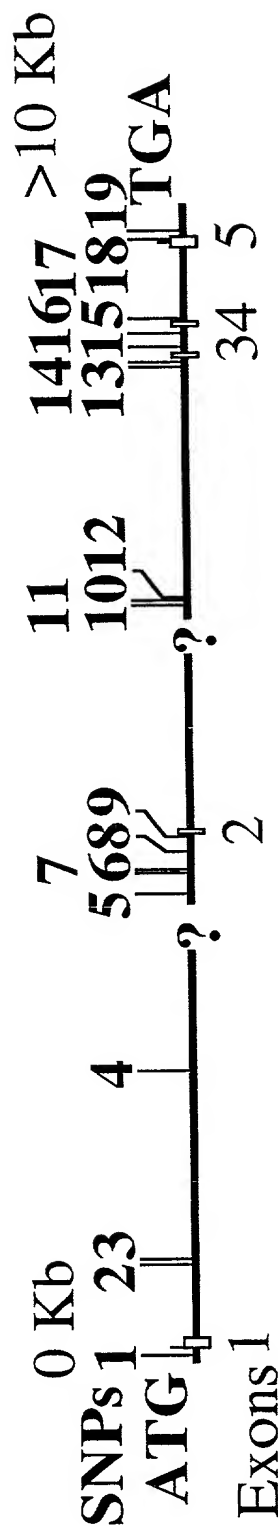


Fig. 241 Tyrosylprotein sulfotransferase 2 (*TPST2*)

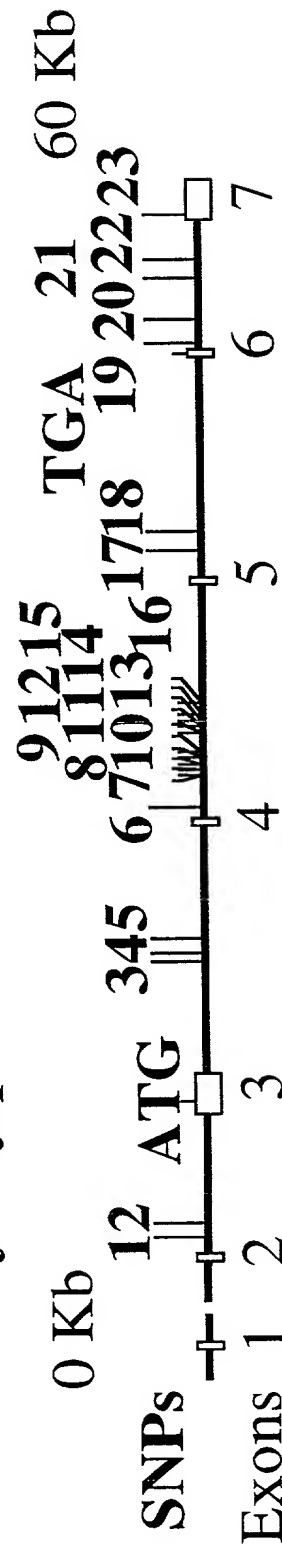


Fig. 242

Cerebroside Sulfotransferase (*CST*)

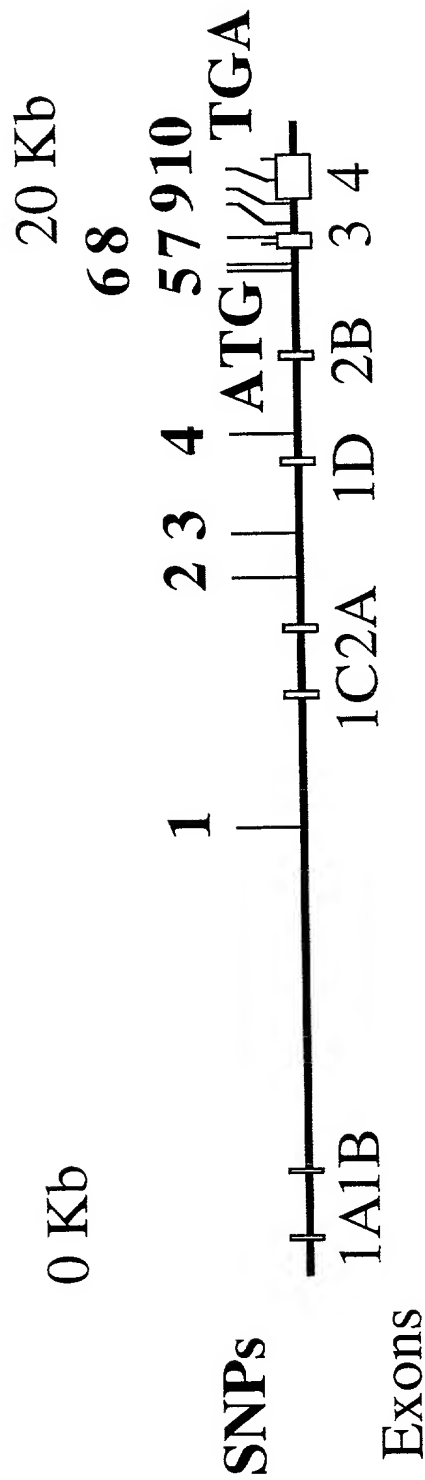


Fig. 243

Thyroid hormone sulfotransferase (ST1B2)

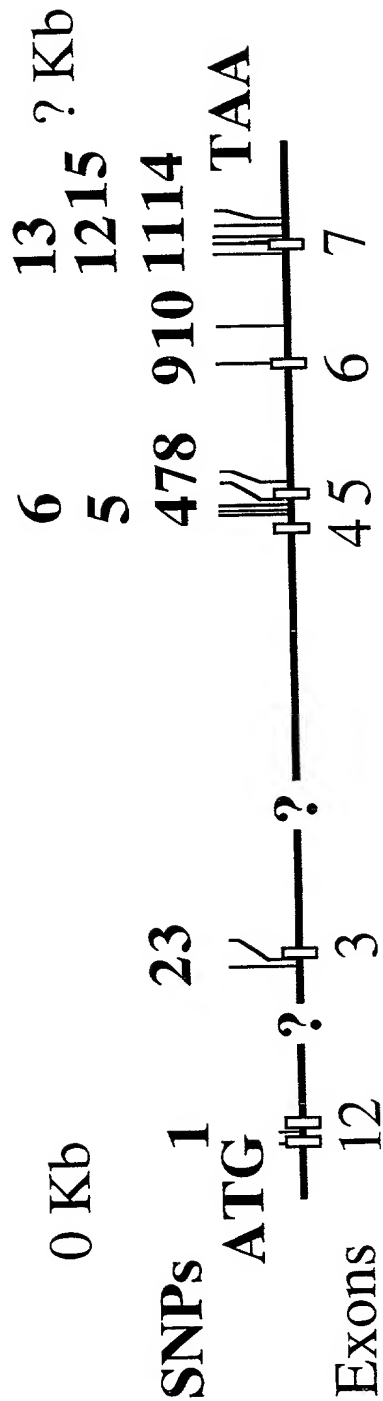


Fig. 244

Carbohydrate sulfotransferase 1 (*CHST1*)

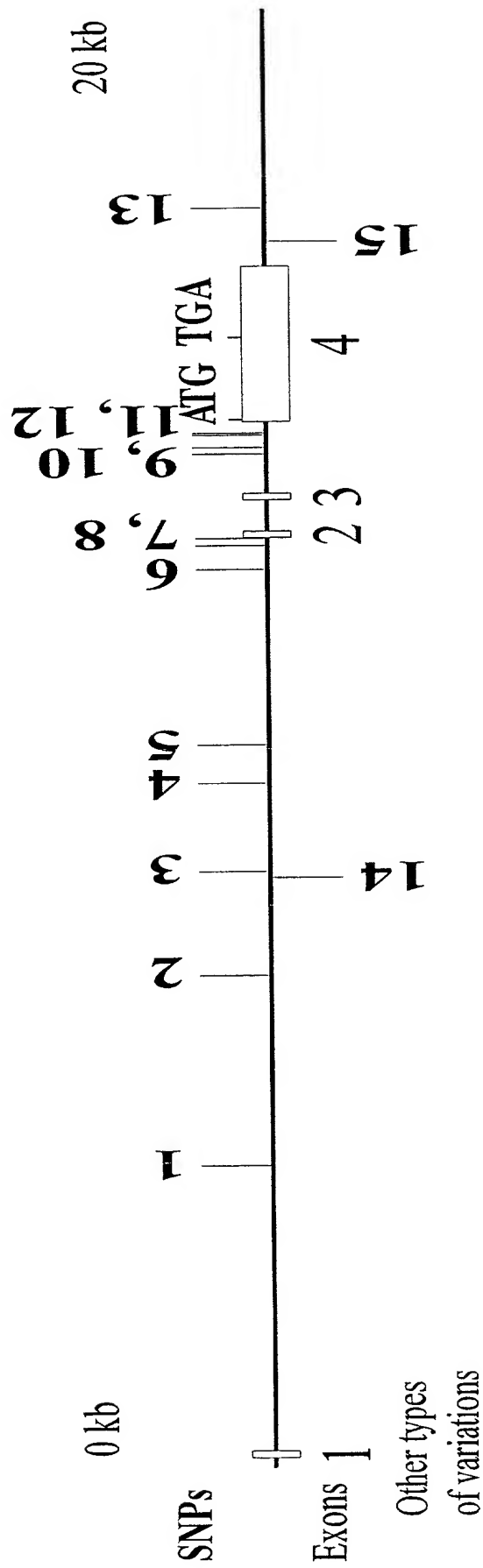


Fig. 245

Carbohydrate sulfotransferase 2 (*CHST2*)

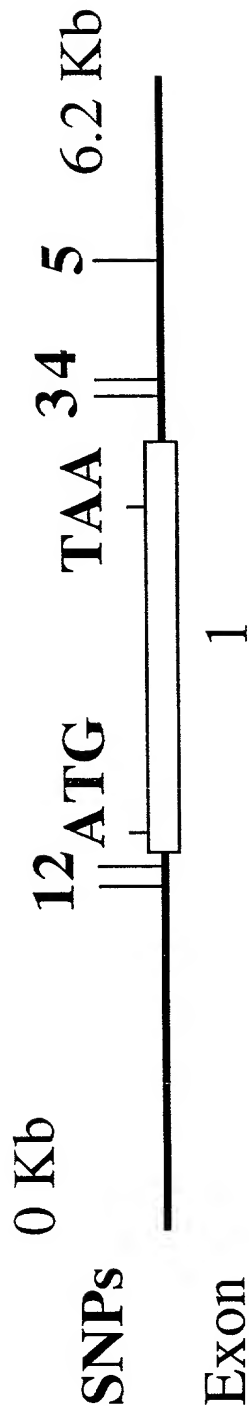


Fig. 247

Carbohydrate sulfotransferase 4 (*CHST4*)

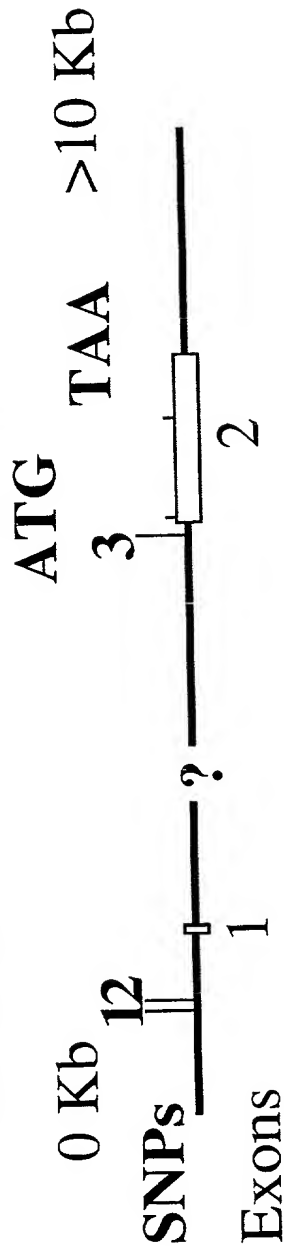


Fig. 248

Carbohydrate sulfotransferase 5 (*CHST5*)

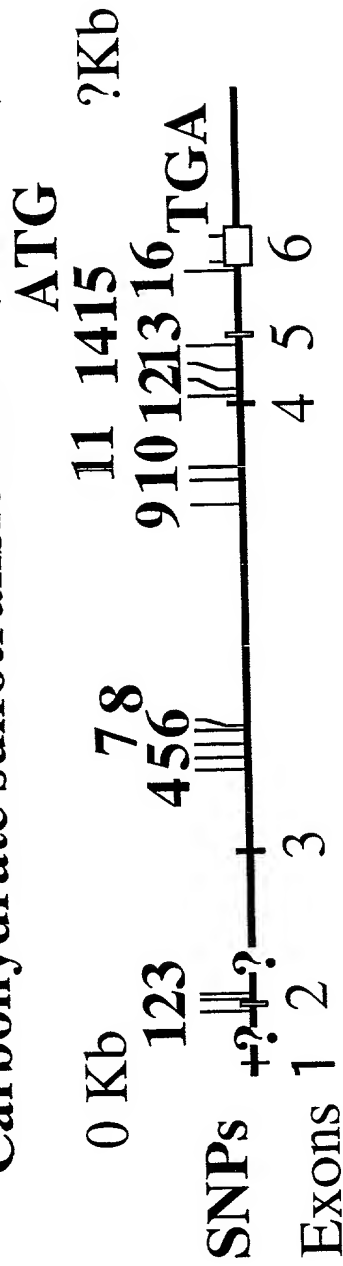


Fig. 249

HNK-sulfotransferase (*HNK-1ST*)

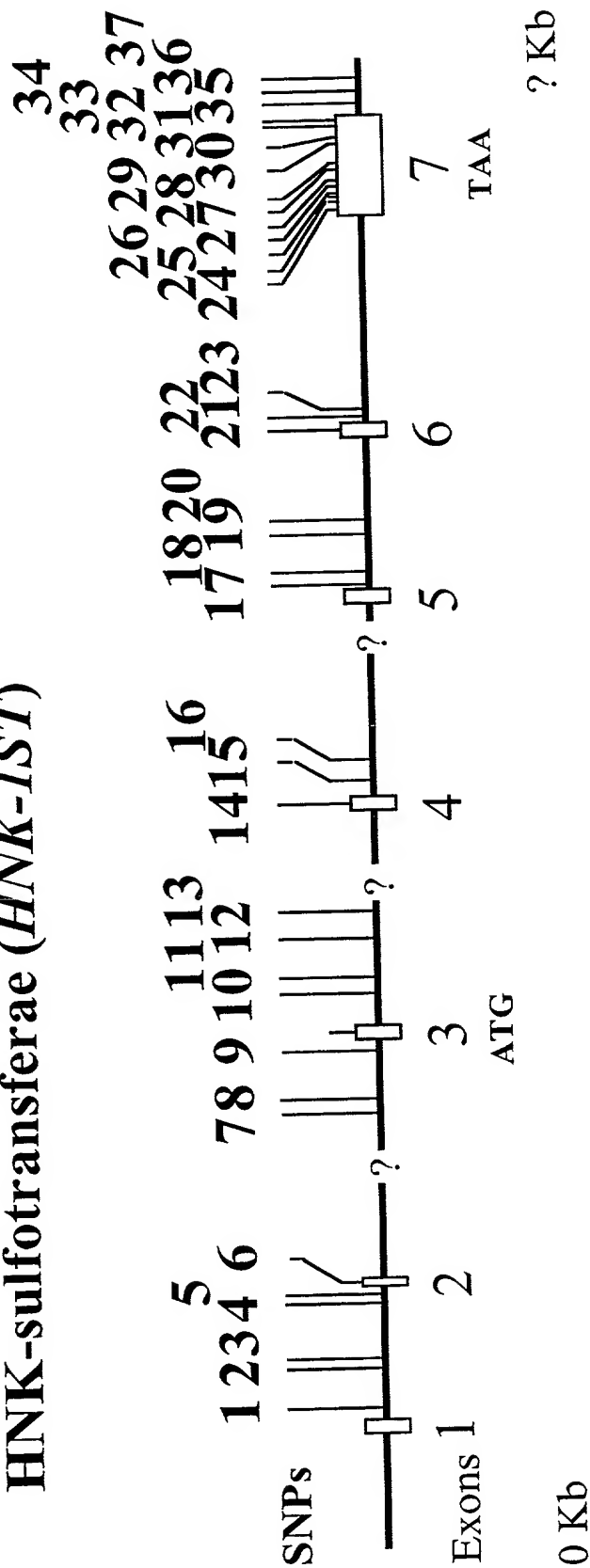


Fig. 250

Estrogen sulfotransferase (*STE*)

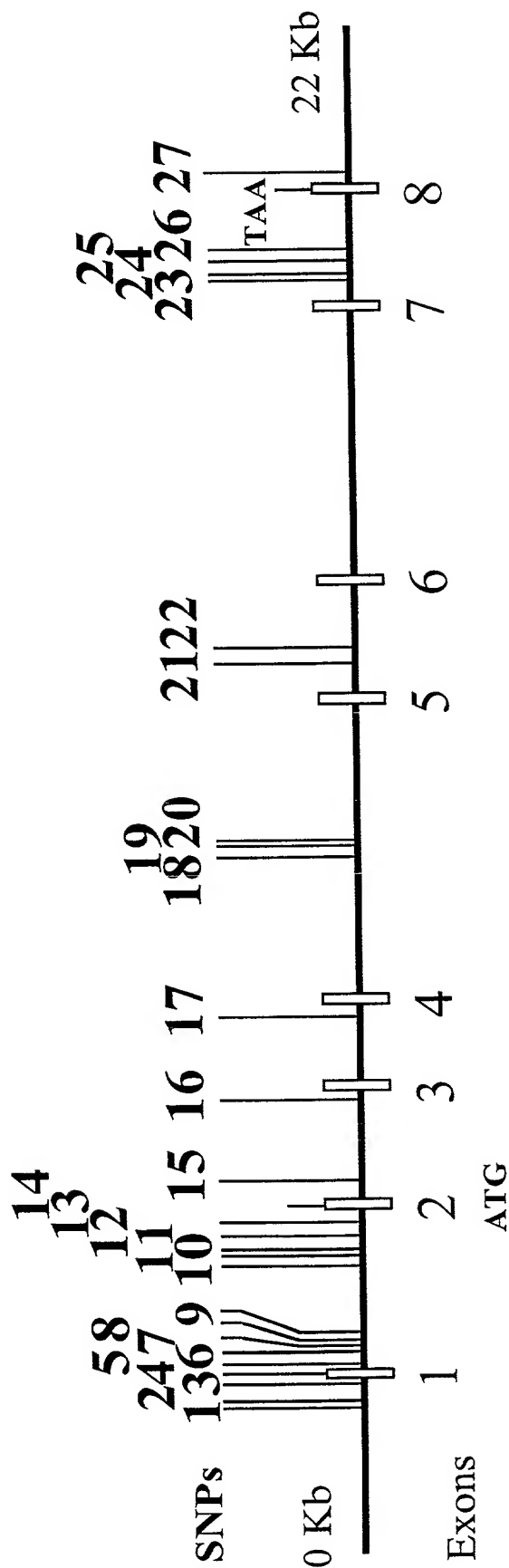


Fig. 251 NAD(P)H:quinone oxidoreductase 1 (*NQO1*)

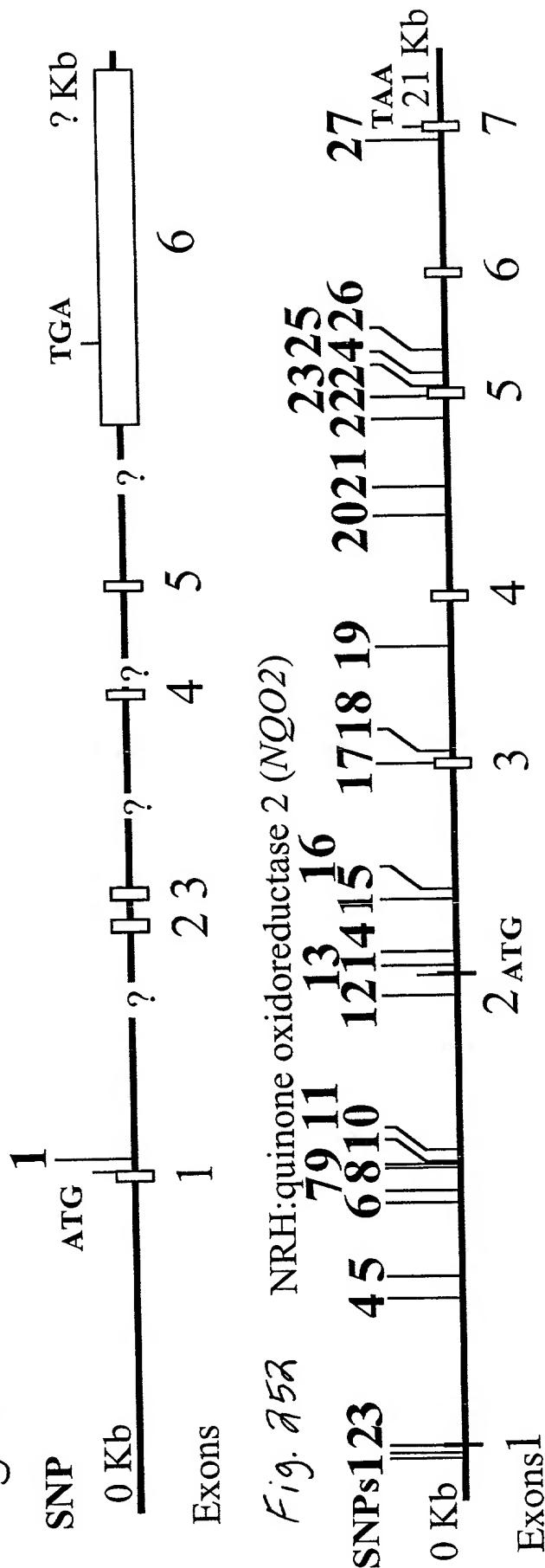


Fig. 252 NRH:quinone oxidoreductase 2 (*NQO2*)

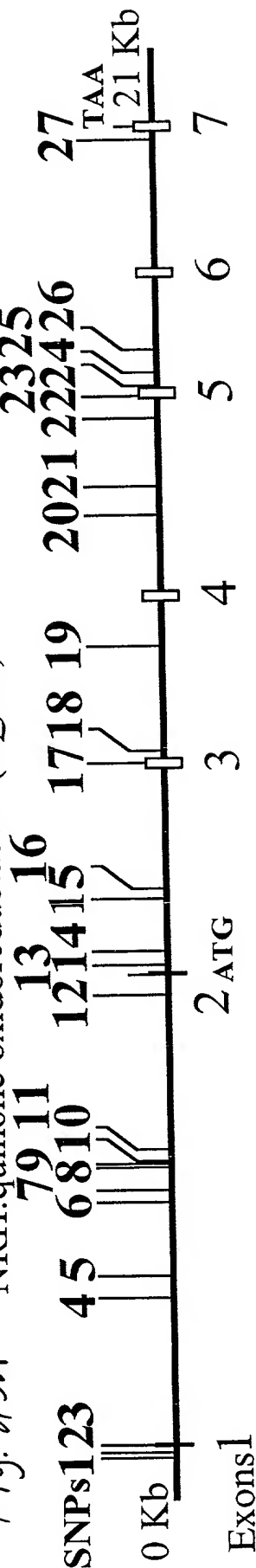


Fig. 253 p53-induced gene 3 (*PIG3*) / Quinone oxidoreductase homolog

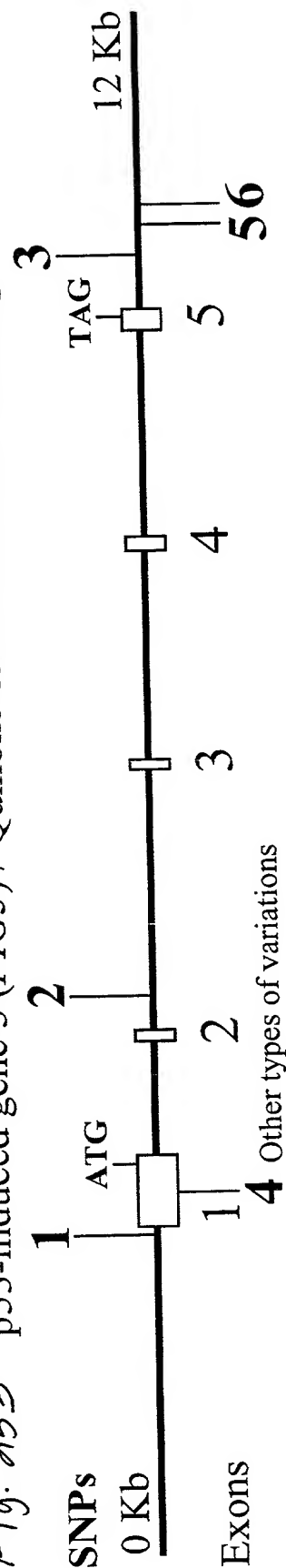


Fig. 254 NADH ubiquinone oxidoreductase 1 alpha subcomplex 1 (NDUFA1)

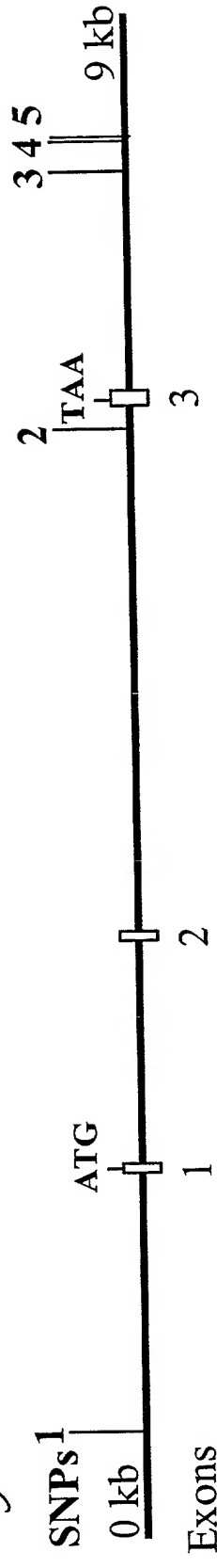


Fig. 255

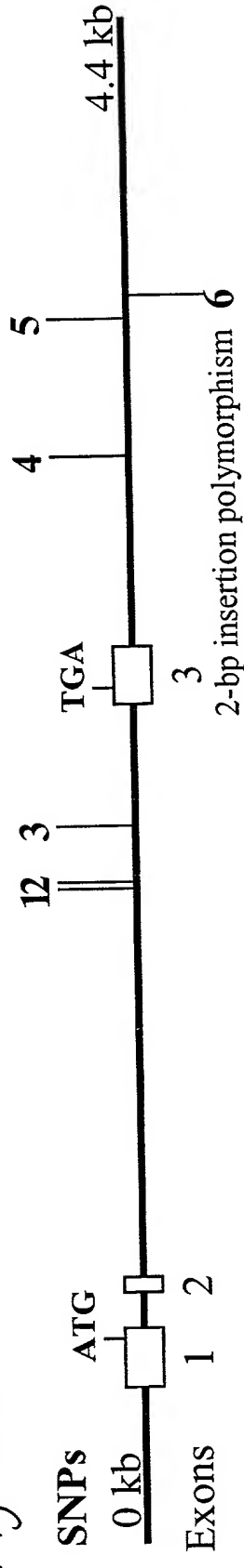
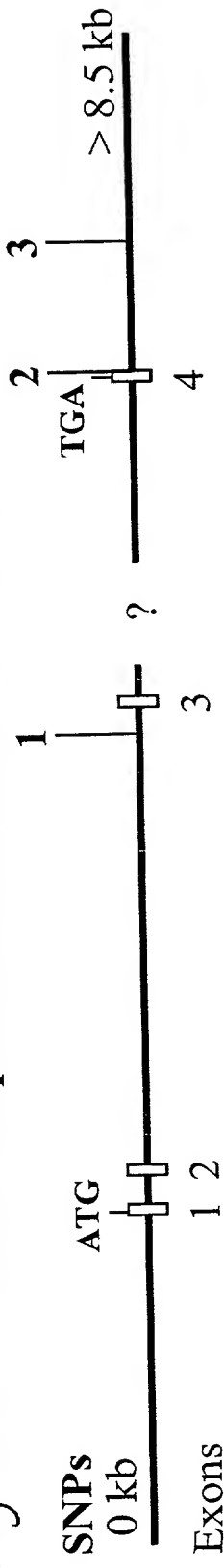


Fig. 256



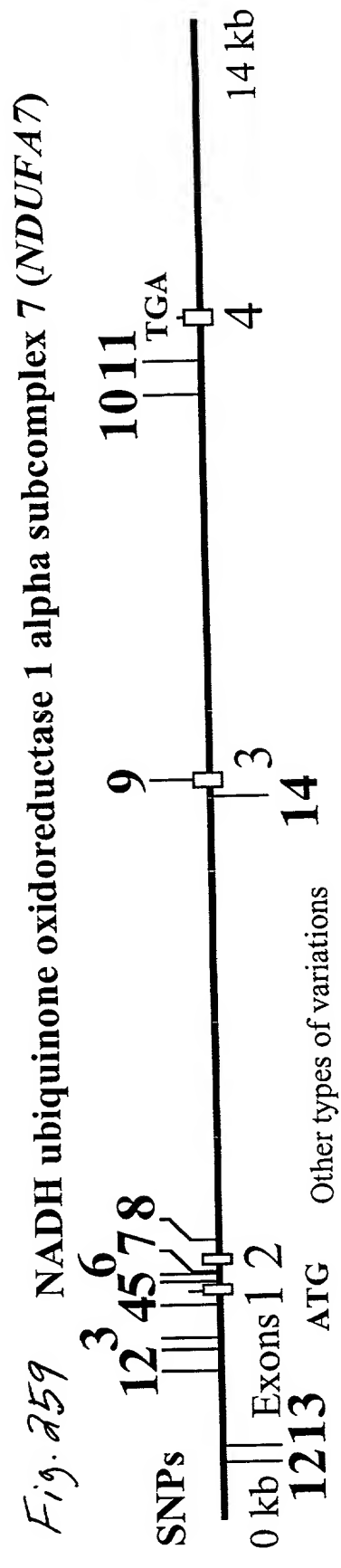
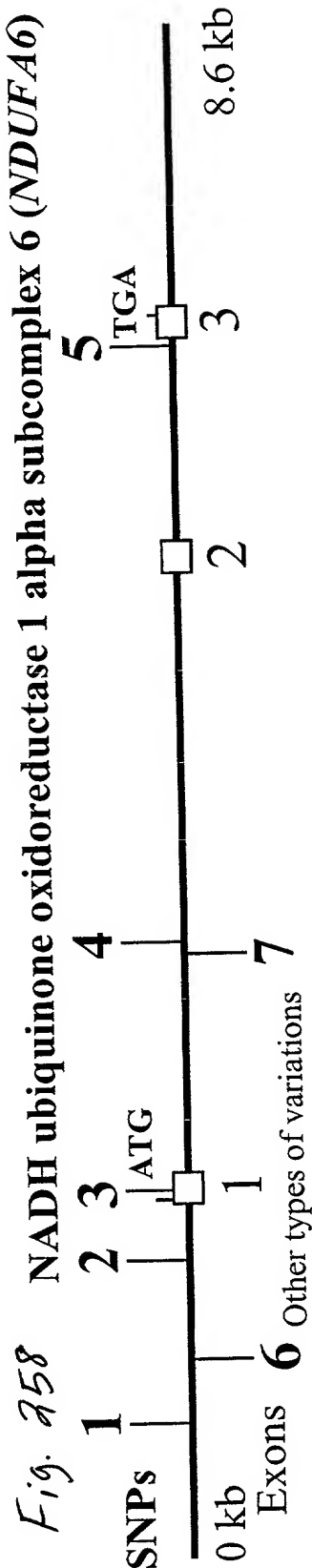
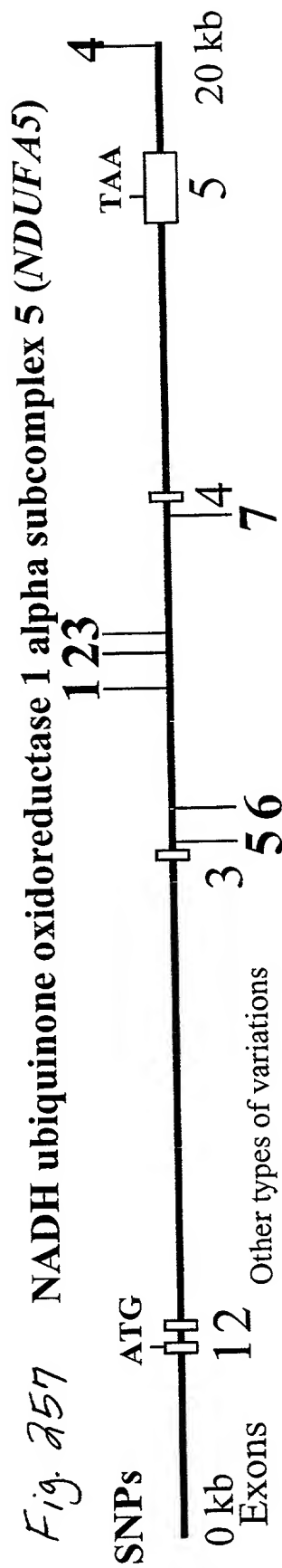


Fig. 261

NADH ubiquinone oxidoreductase 1 alpha subcomplex 9 (*NDUF A9*)

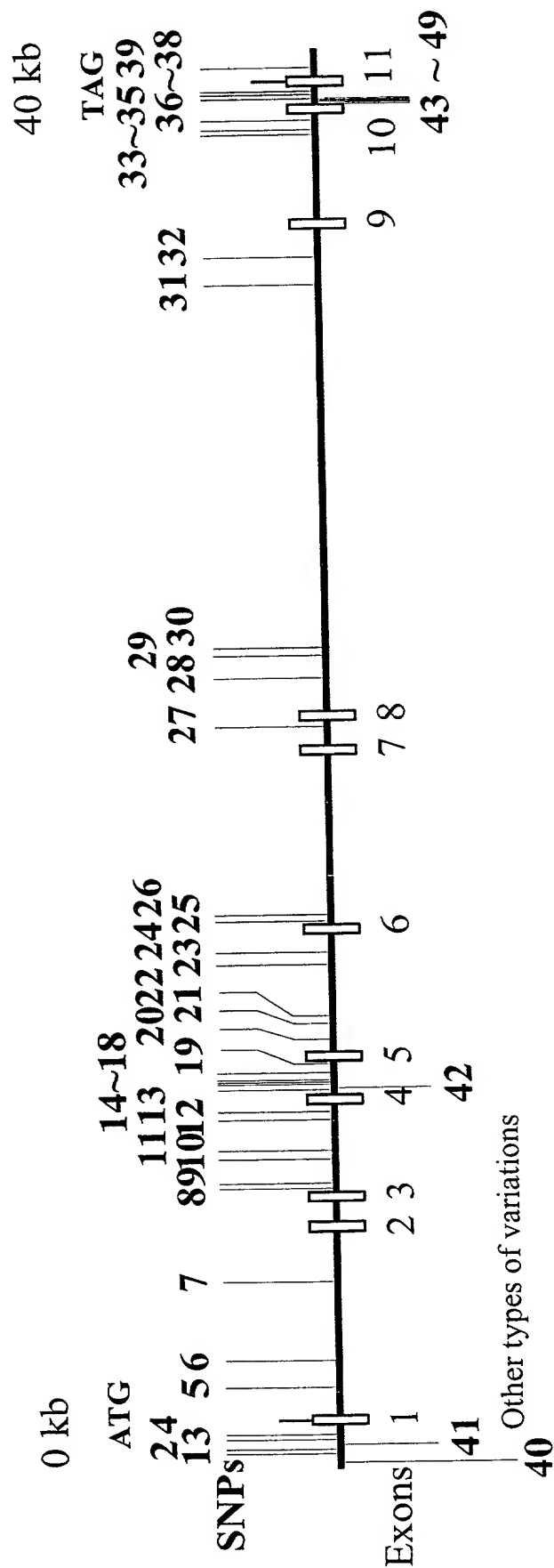


Fig. 262

NADH: ubiquinone oxidoreductase A 10 (NDUFA10)

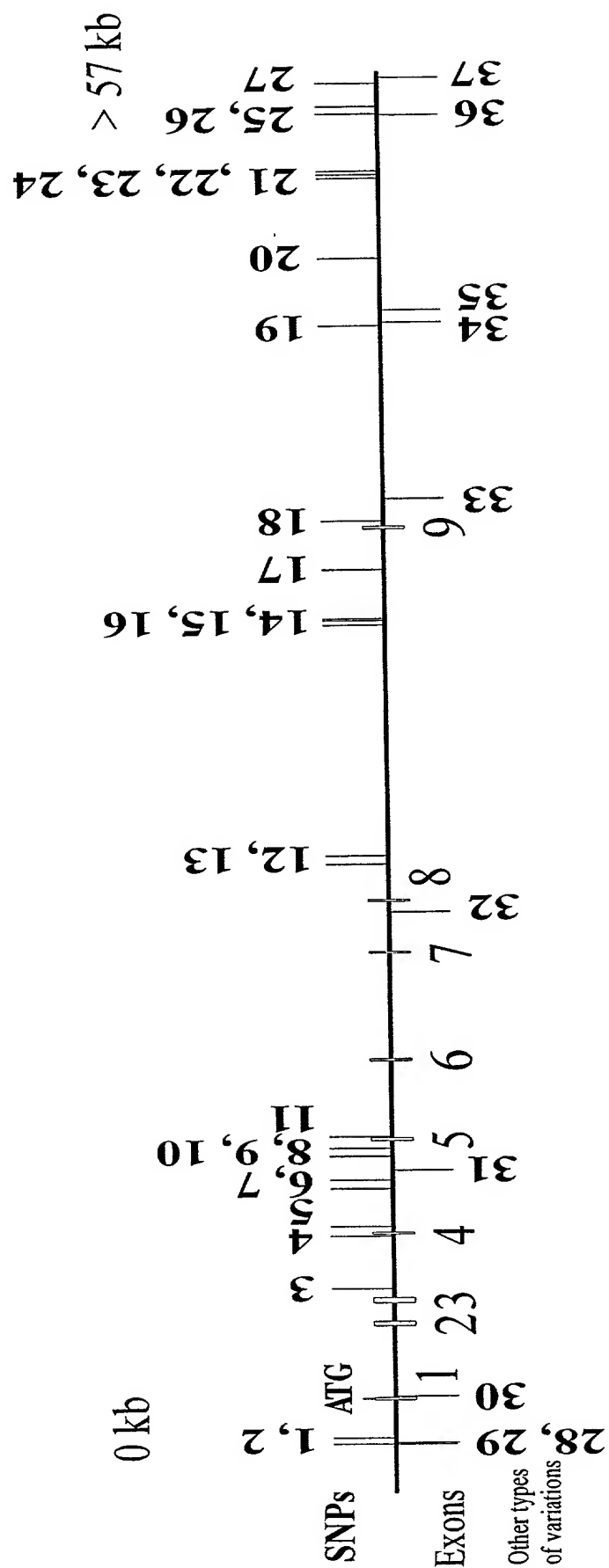


Fig. 263
NADH ubiquinone oxidoreductase 1 alpha/beta subcomplex 1
(*NDUFAB1*)

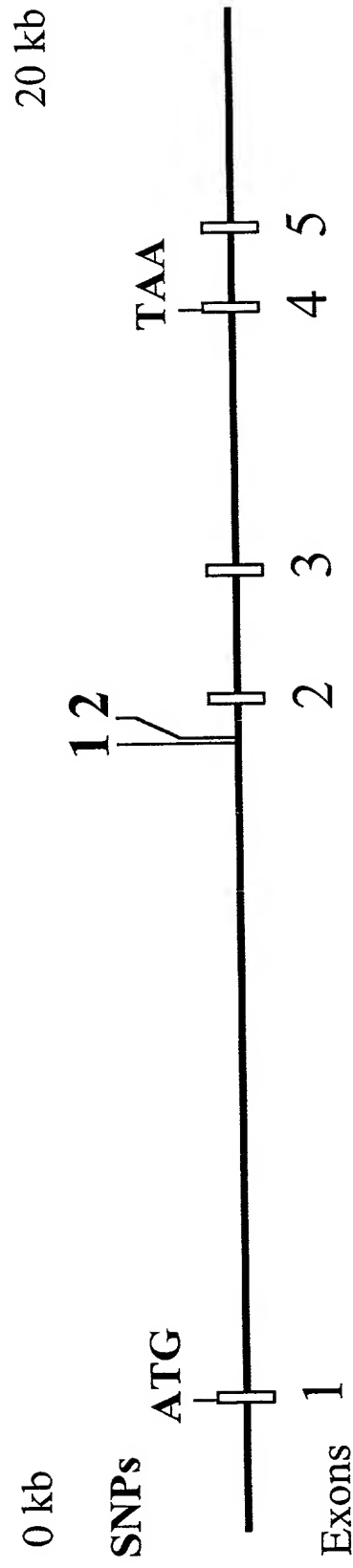


Fig. 264

NADH ubiquinone oxidoreductase 1 beta subcomplex 3 (*NDUFB3*)

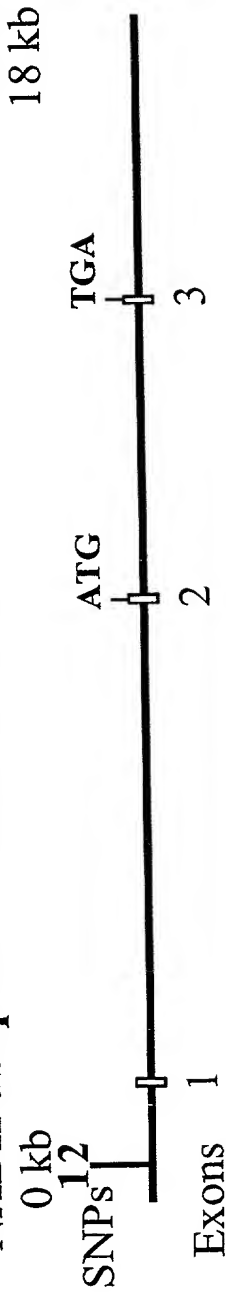


Fig. 265

NADH ubiquinone oxidoreductase 1 beta subcomplex 5 (*NDUFB5*)

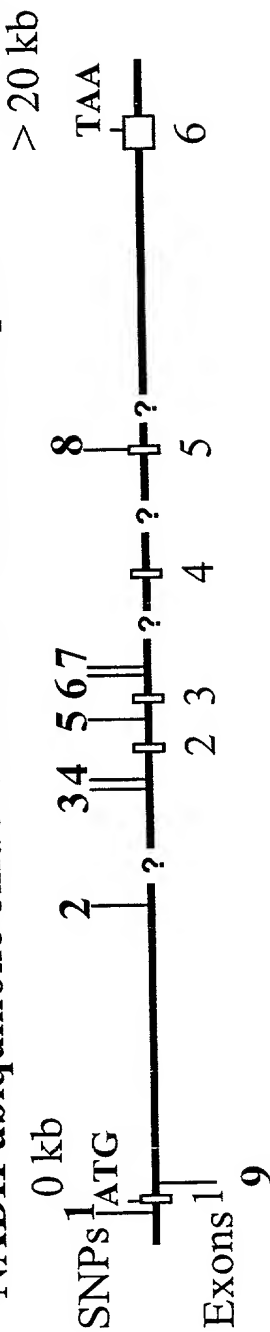


Fig. 266

NADH ubiquinone oxidoreductase 1 beta 7 (*NDUFB7*)

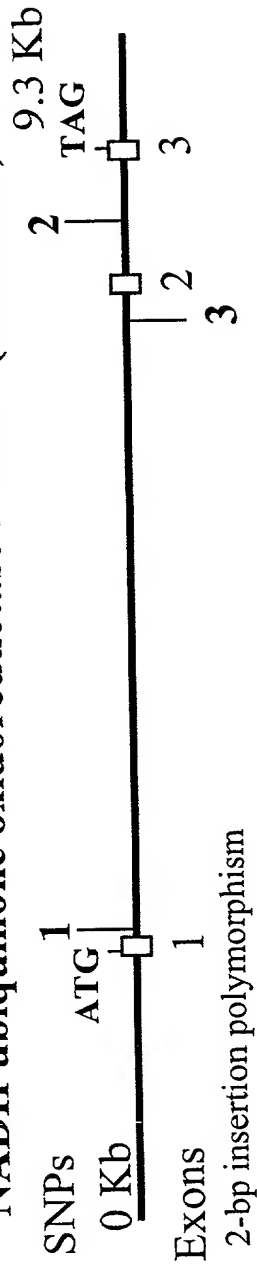


Fig. 267 NADH ubiquinone oxidoreductase Fe-S protein 1 (*NDUFS1*)

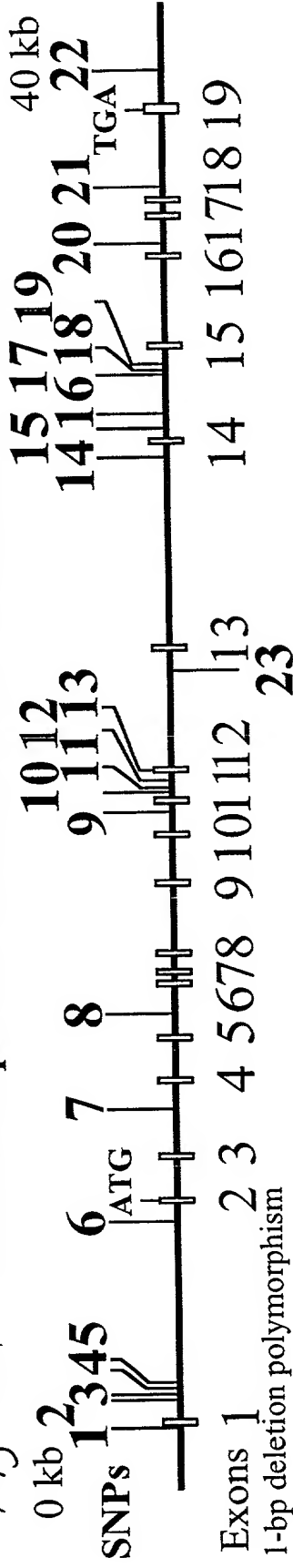


Fig. 268 NADH ubiquinone oxidoreductase Fe-S protein 3 (*NDUFS3*)

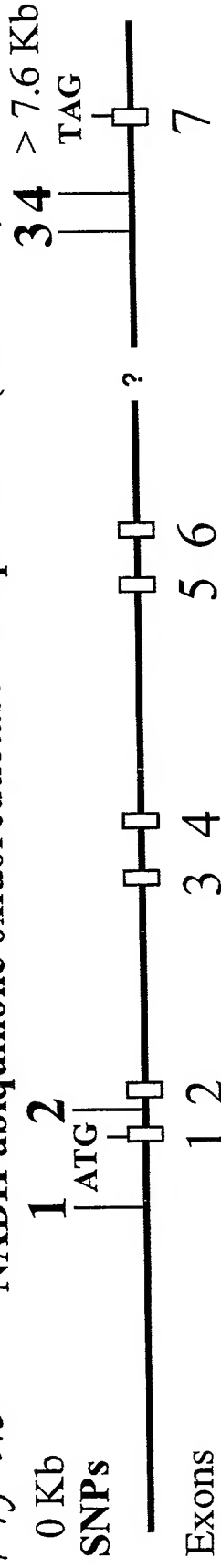


Fig. 269 NADH ubiquinone oxidoreductase Fe-S protein 4 (*NDUFS4*)

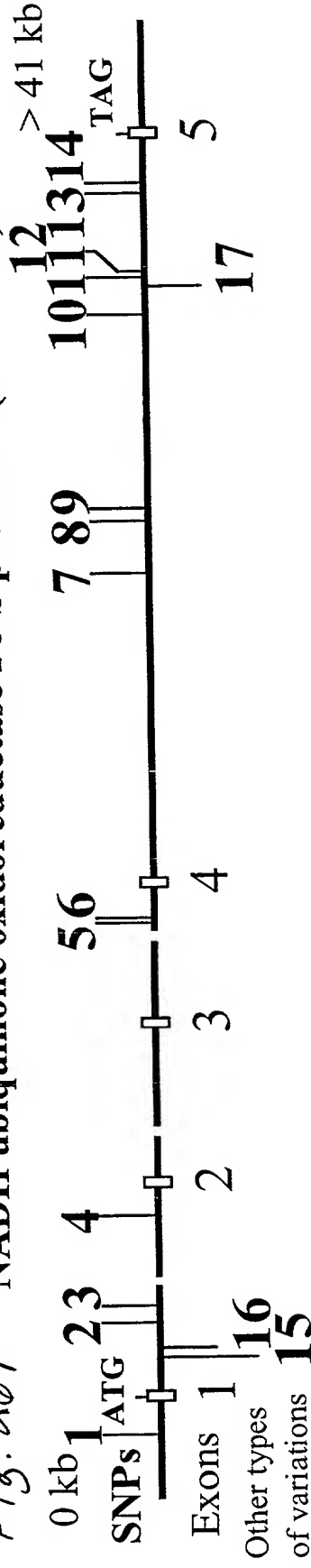


Fig. 270 NADH ubiquinone oxidoreductase Fe-S protein 5 (*NDUFS5*)

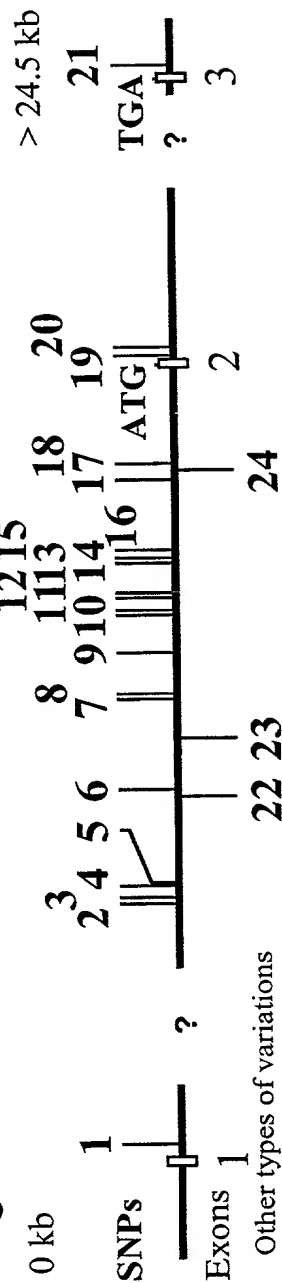


Fig. 271 NADH ubiquinone oxidoreductase Fe-S protein 6 (*NDUFS6*)

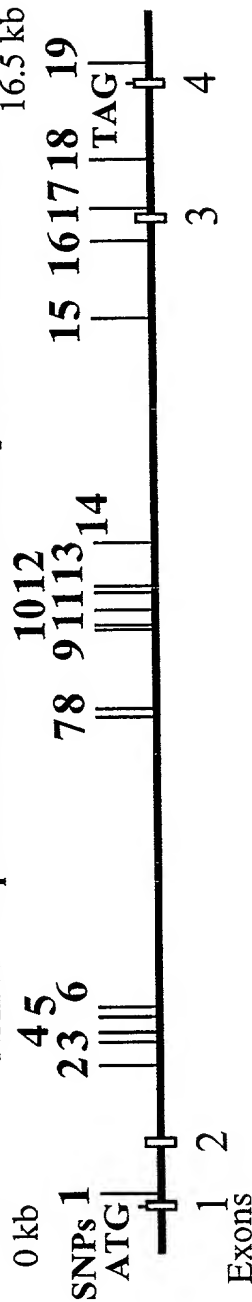


Fig. 272 NADH ubiquinone oxidoreductase Fe-S protein 8 (*NDUFS8*)

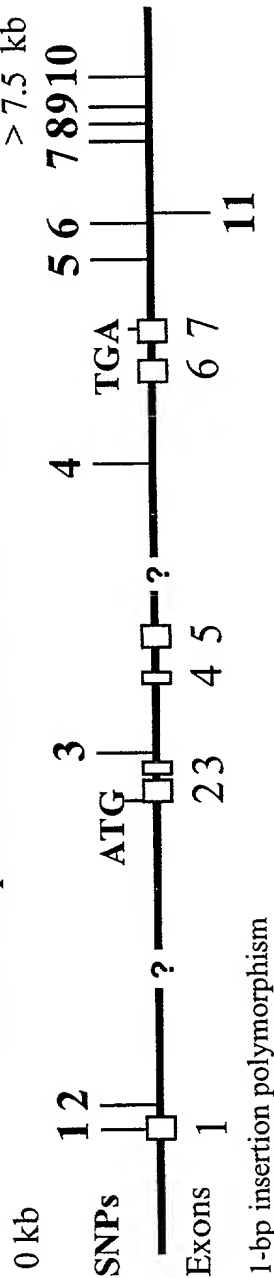


Fig. 273

NADH: ubiquinone dehydrogenase flavoprotein 1 (*NDUFV1*)

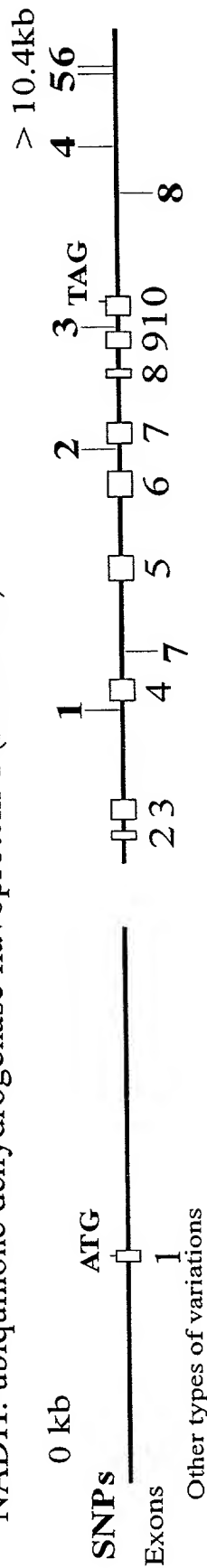


Fig. 274

NADH: ubiquinone oxidoreductase flavoprotein 2 (*NDUFV2*)

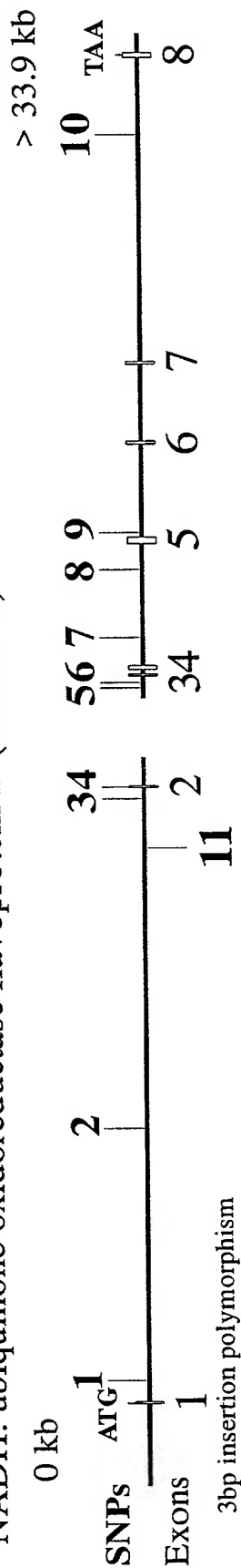


Fig. 275

NADH: ubiquinone oxidoreductase flavoprotein 3 (*NDUFV3*)

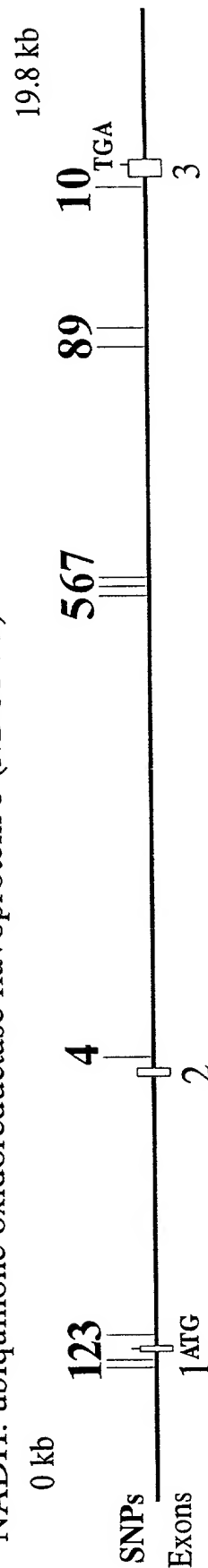


Fig. 276

Gamma-glutamyltransferase 1 (GGT1)

ACCESSION D87002.1

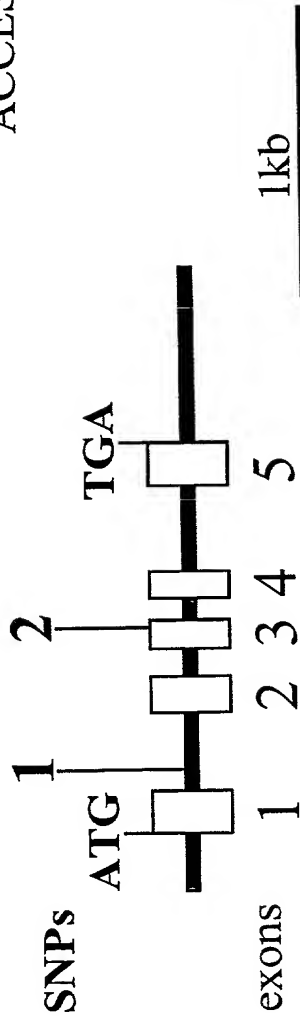


Fig. 277

Transglutaminase 1 (TGMI)

ACCESSION M98447.1

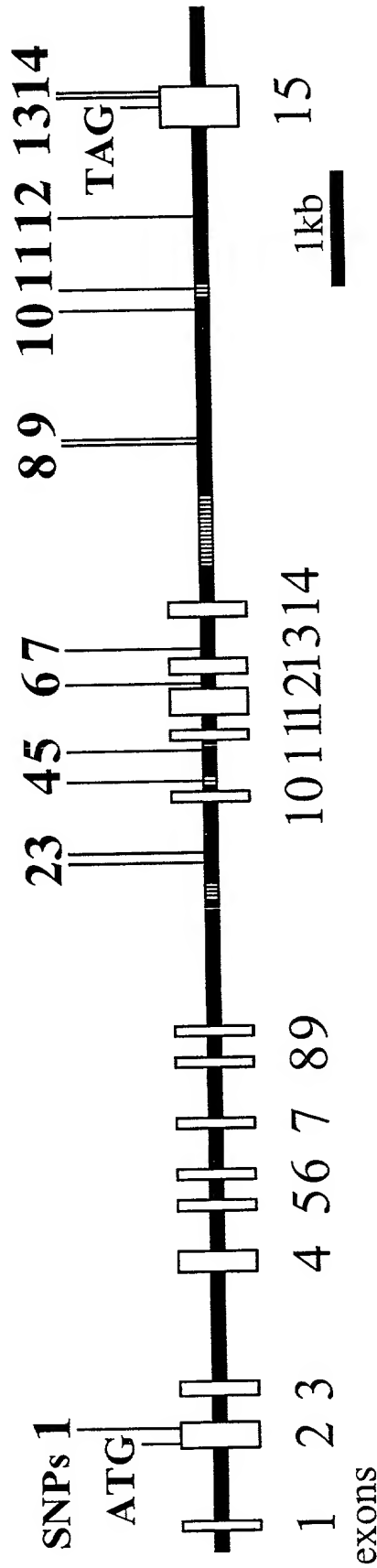


Fig. 278

Cytochrome P450, subfamily I, polypeptide 1 (CYP1A1)

ACCESSION X04300.1 AC020705.4

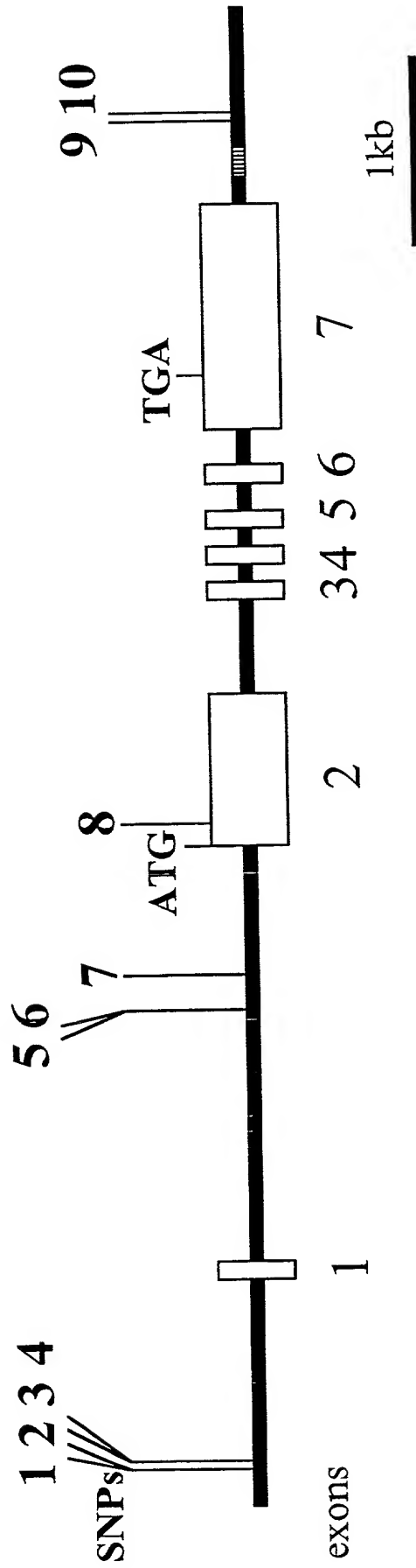


Fig. 279

Cytochrome P450, subfamily 1, polypeptide 2 (CYP1A2)

ACCESSION AC020705.4

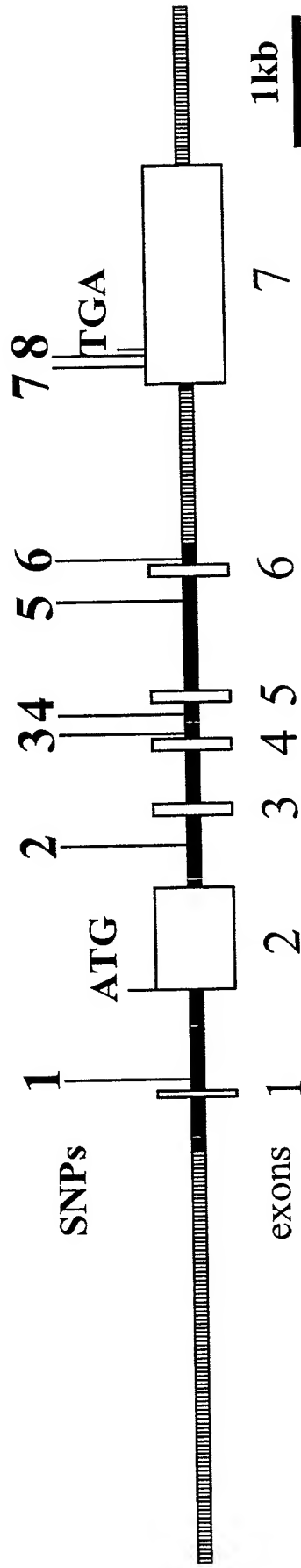


Fig. 280

Cytochrome P450, subfamily 1, polypeptide 1 (CYP1B1)

ACCESSION AC009229.4

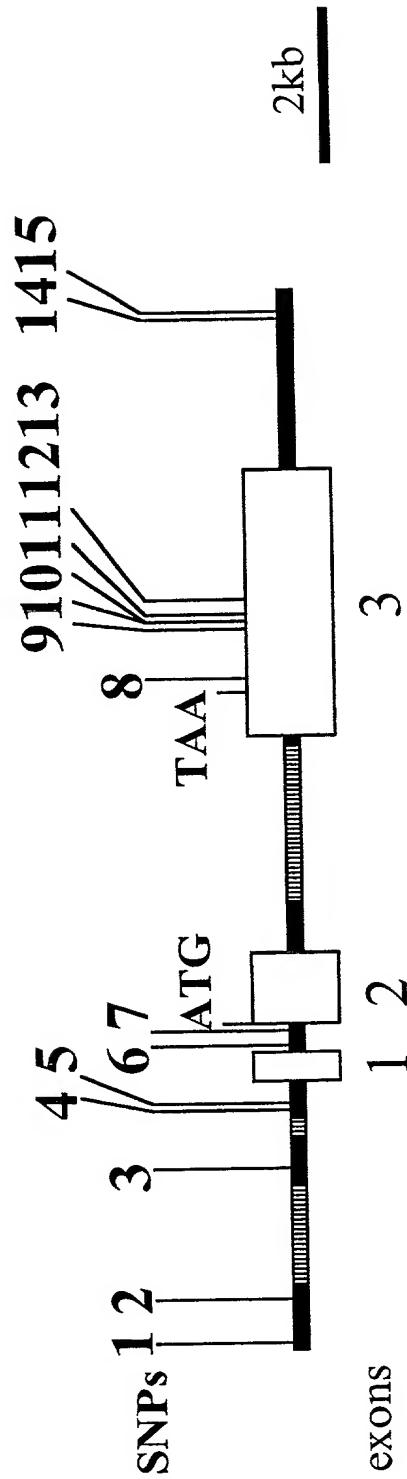


Fig. 281

Cytochrome P450, subfamily IIIA, polypeptide 4 (CYP3A4)

ACCESSION AF280107.1

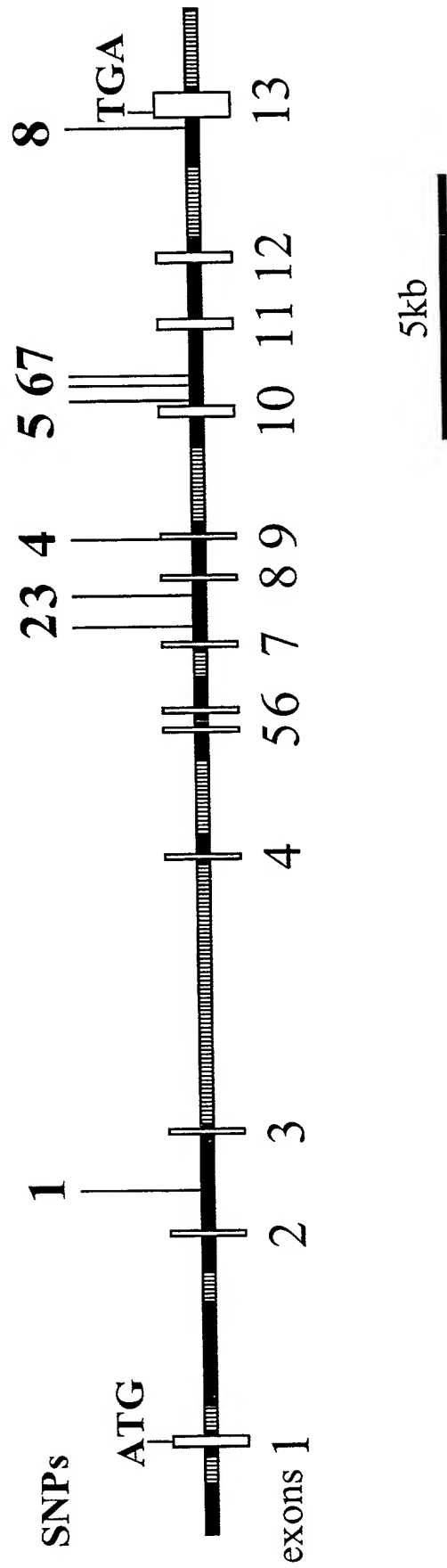


Fig. 282

Cytochrome P450, subfamily IIIA, polypeptide 5 (CYP3A5)

ACCESSION AC005020.5

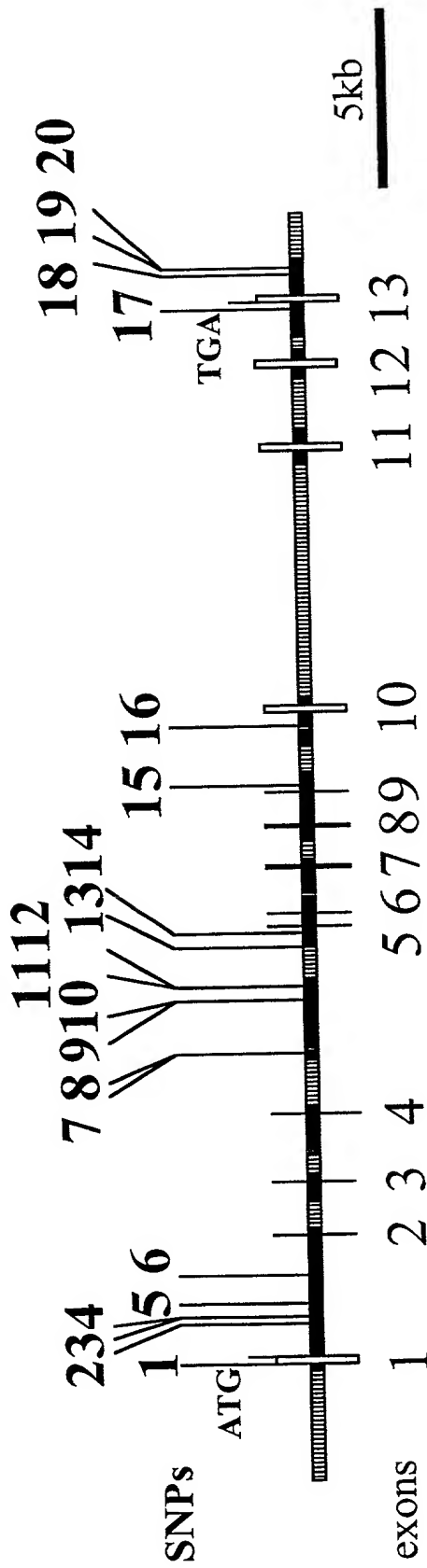


Fig. 283

Cytochrome P450, subfamily IIIA, polypeptide 7 (CYP3A7)

ACCESSION AF280107.1

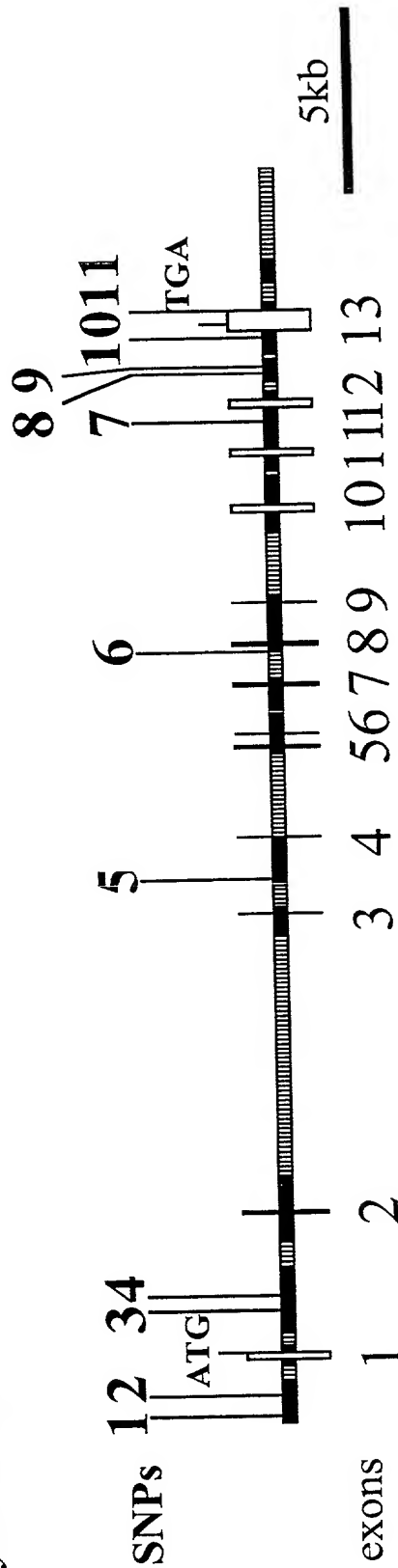


Fig. 784 Cytochrome P450, subfamily IIIA, polypeptide 43 (CYP3A43)

ACCESSION AC011904.3

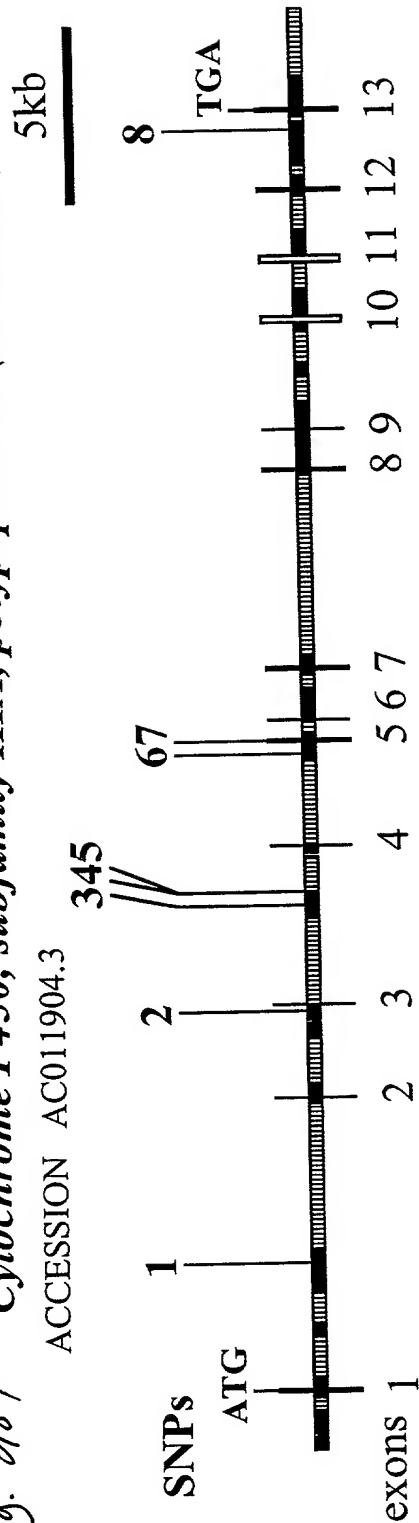


Fig. 785 Cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1)

ACCESSION AL356793.10

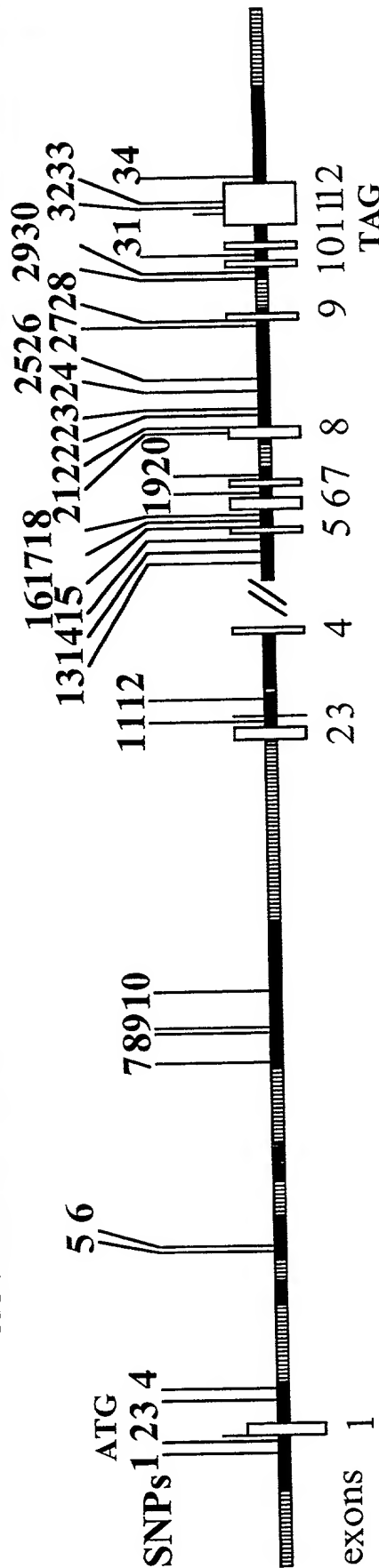


Fig. 286 Cytochrome P450, subfamily IVF, polypeptide 2 (CYP4F2) ACCESSION AC005336.1

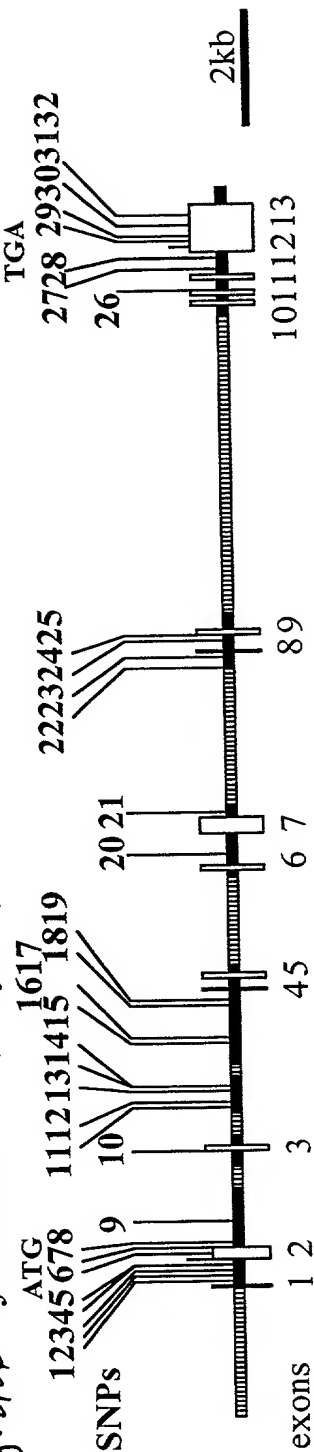


Fig. 287 Cytochrome P450, subfamily IVF, polypeptide 3 (CYP4F3) 2425262728 ACCESSION AD000685.1

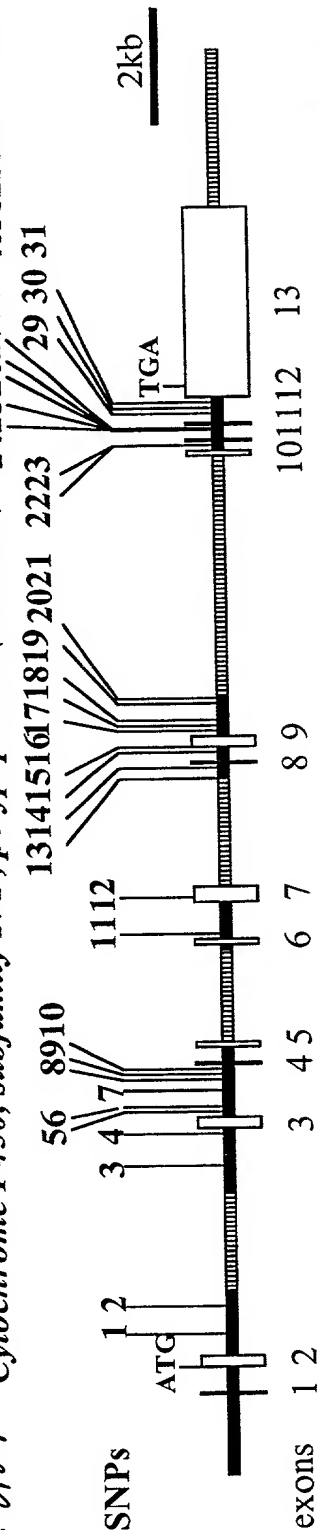


Fig. 288 Cytochrome P450, subfamily IVF, polypeptide 8 (CYP4F8) ACCESSION AC068845.3

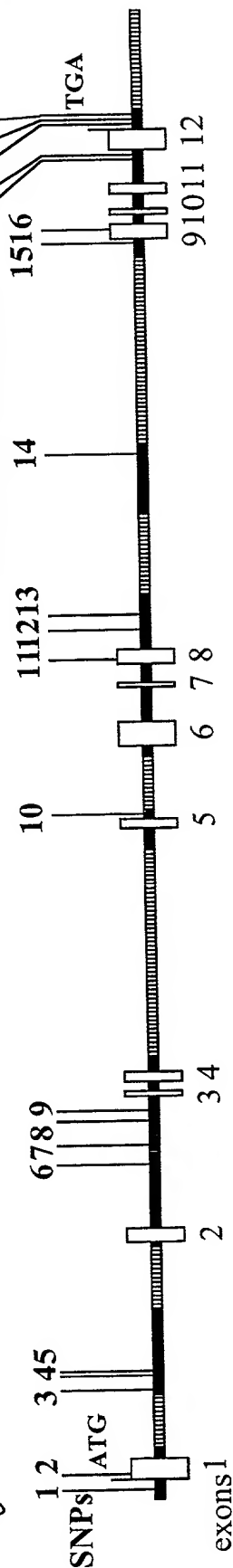


Fig. 289 Cytochrome P450, subfamily XXVIIA, polypeptide 1 (CYP27A1)

ACCESSION AC009974.7

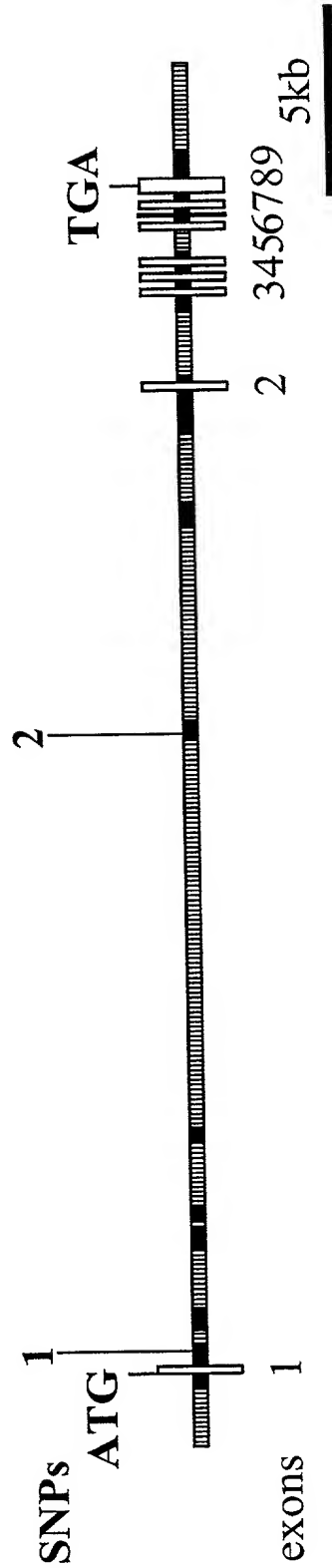


Fig. 290 Cytochrome P450, subfamily XXVIIIB, polypeptide 1 (CYP27B1)

ACCESSION AC025165.27

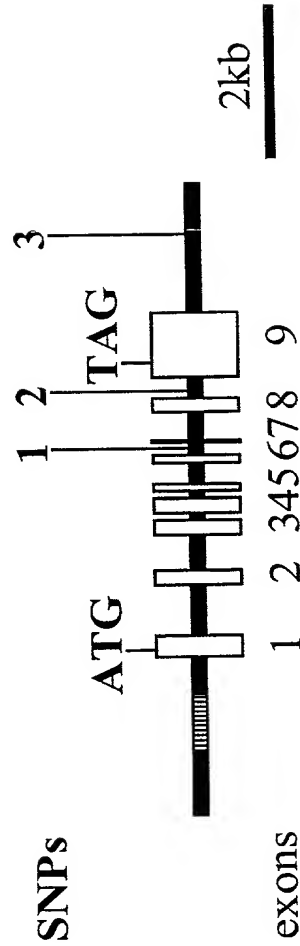


Fig. 291 Arylacetamide deacetylase (AADAC) AC068647.4

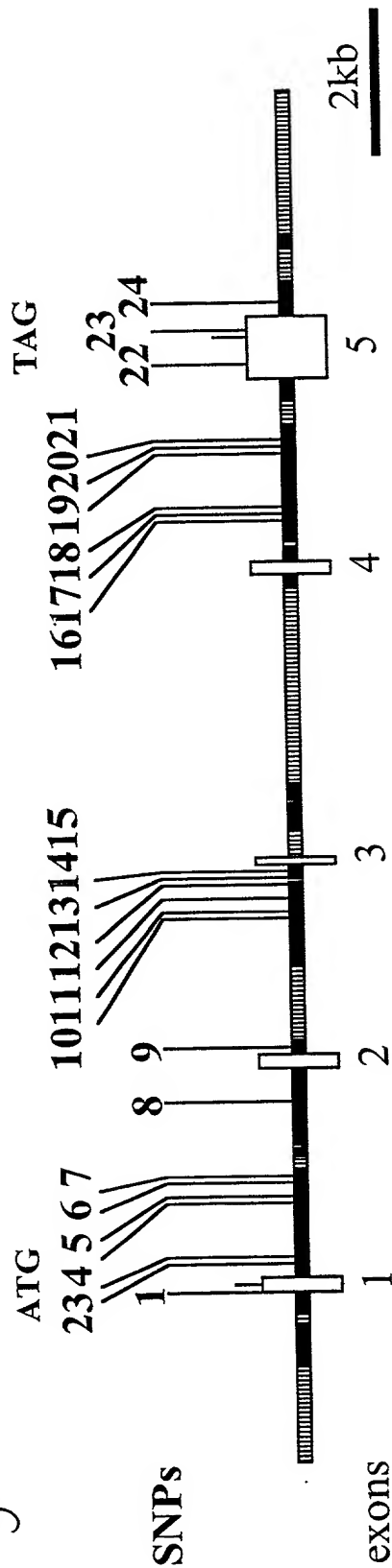


Fig. 292 Carboxylesterase 1 (CES1) AC007602.4

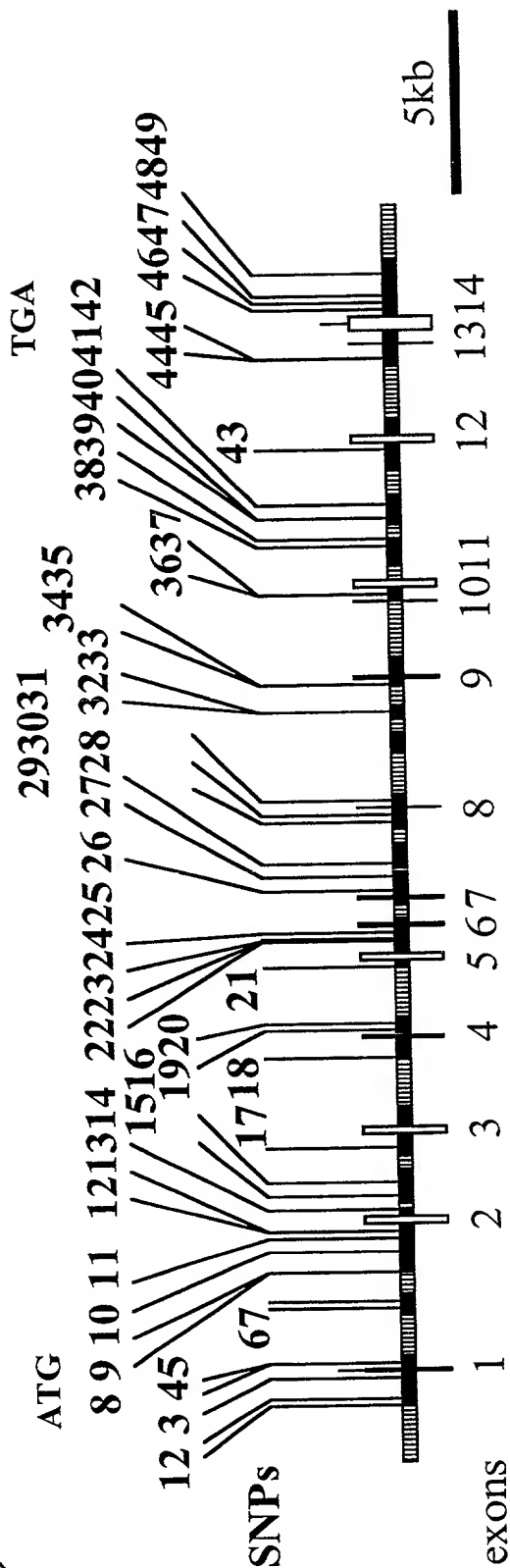


Fig. 293

Carboxylesterase 2 (CES2)

ACCESSION AC027131.4

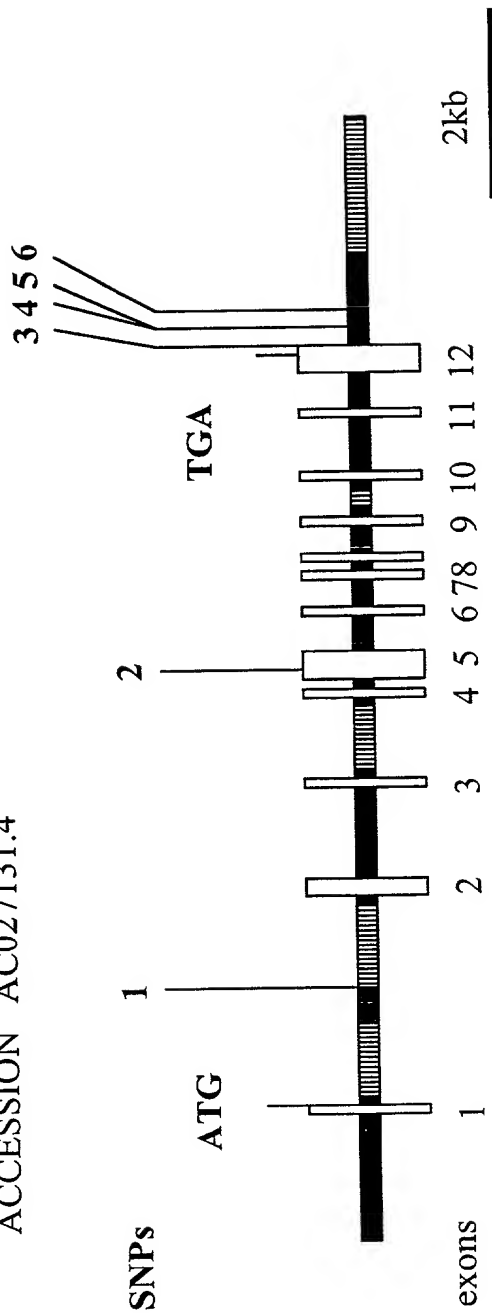


Fig. 294 *Granzyme A (GZMA)*

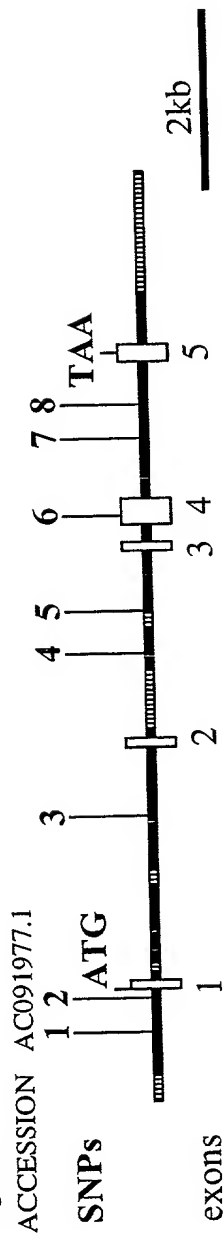


Fig. 295 *Granzyme B (GZMB)*

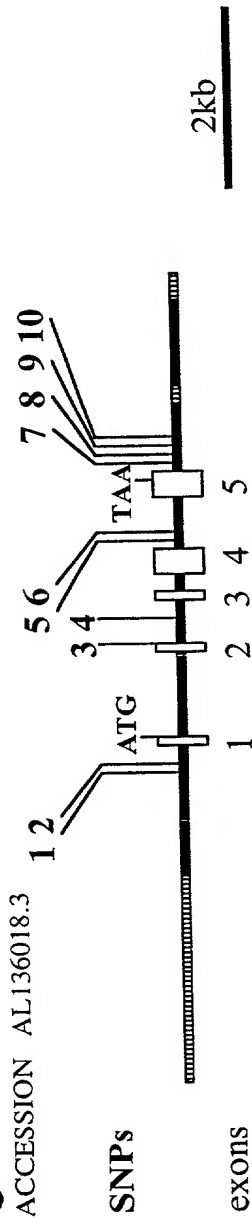


Fig. 296 *Esterase D (ESD)*

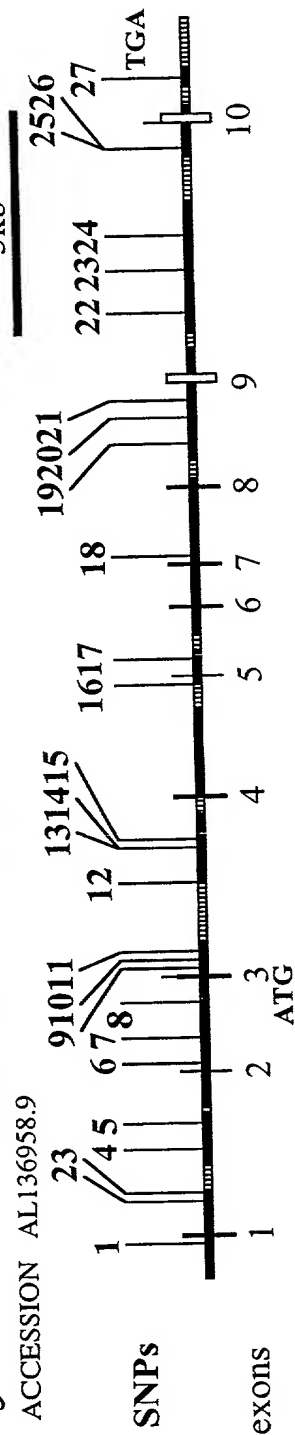


Fig. 297A *Carboxyl ester lipase (CEL)*
 ACCESSION AL138750.1 AL162417.20 AF072711.1

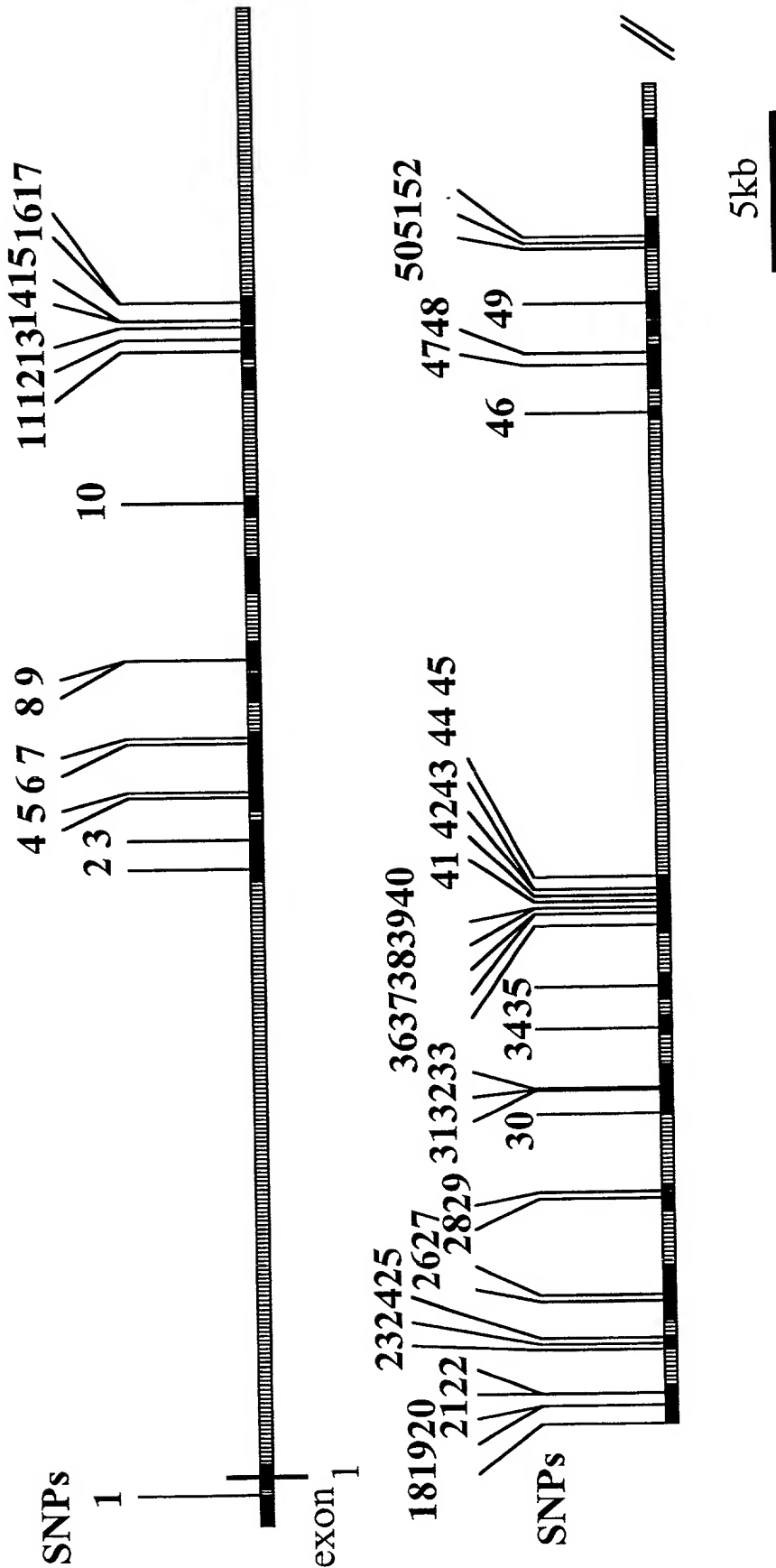


Fig. 297B

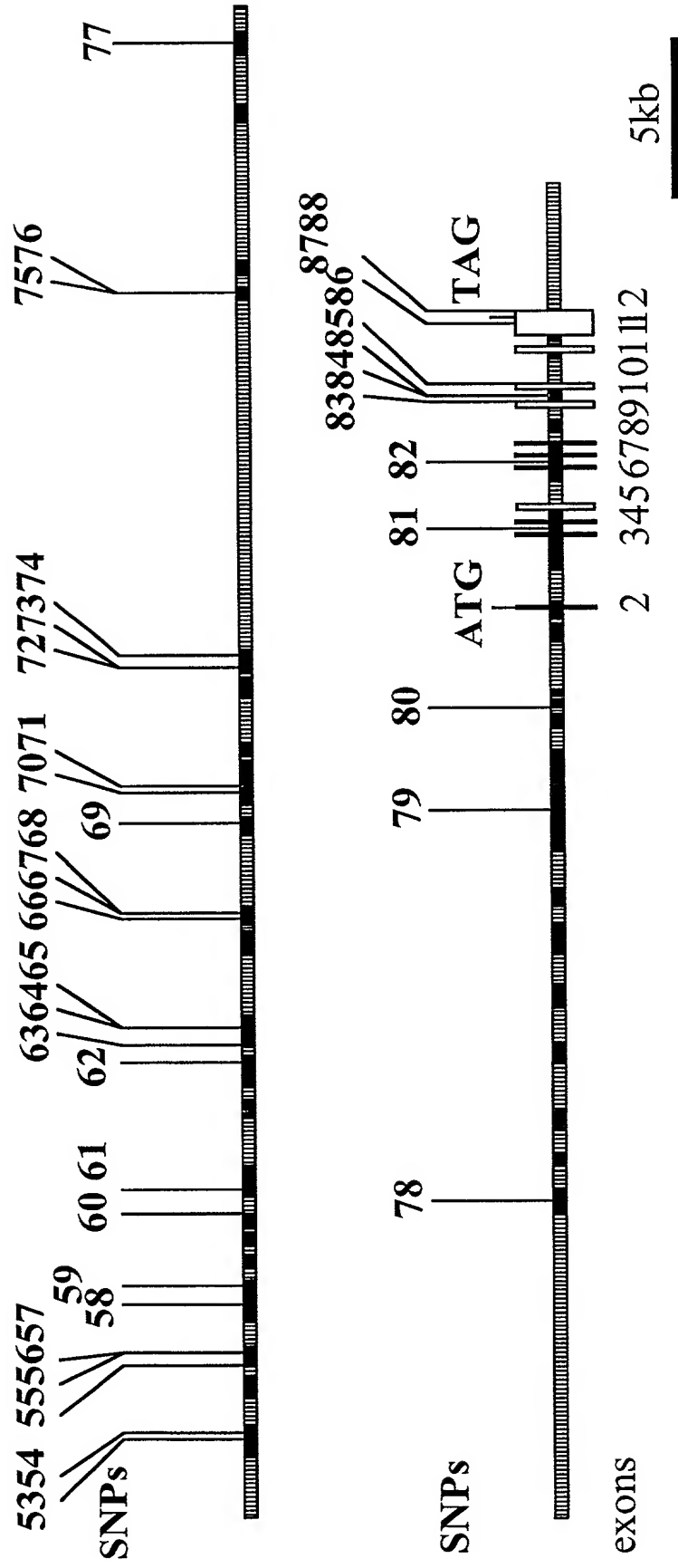


Fig. 798

Interleukin 17
(cytotoxic T-lymphocyte-associated serine esterase 8) (IL17)

ACCESSION AL355513.11

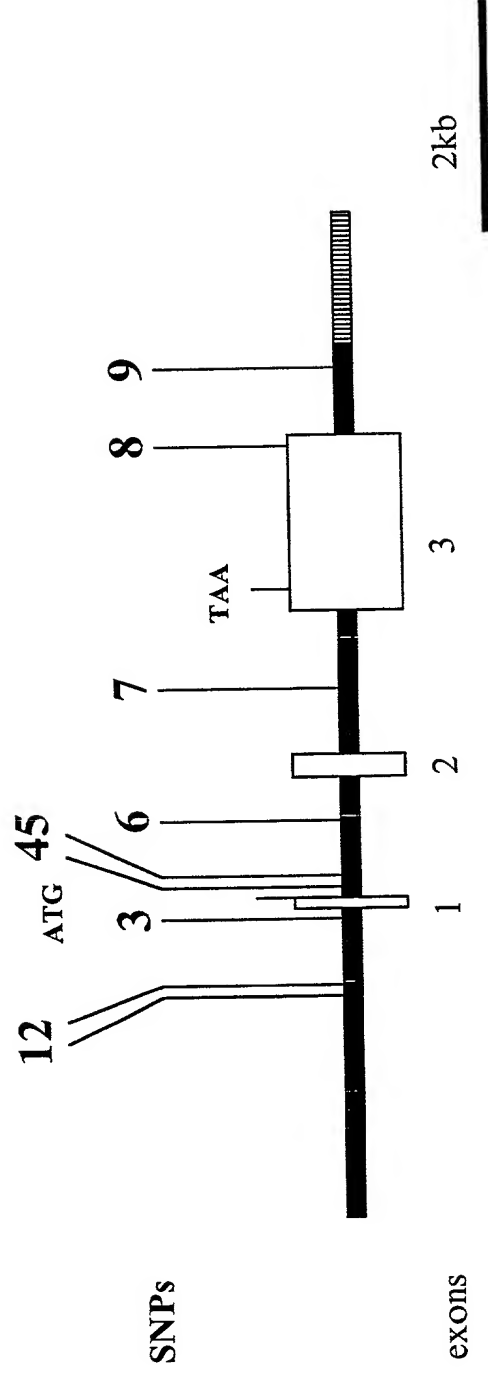


Fig. 299 Ubiquitin carboxyl-terminal esterase L3 (UCHL3)

ACCESSION AL137244.28

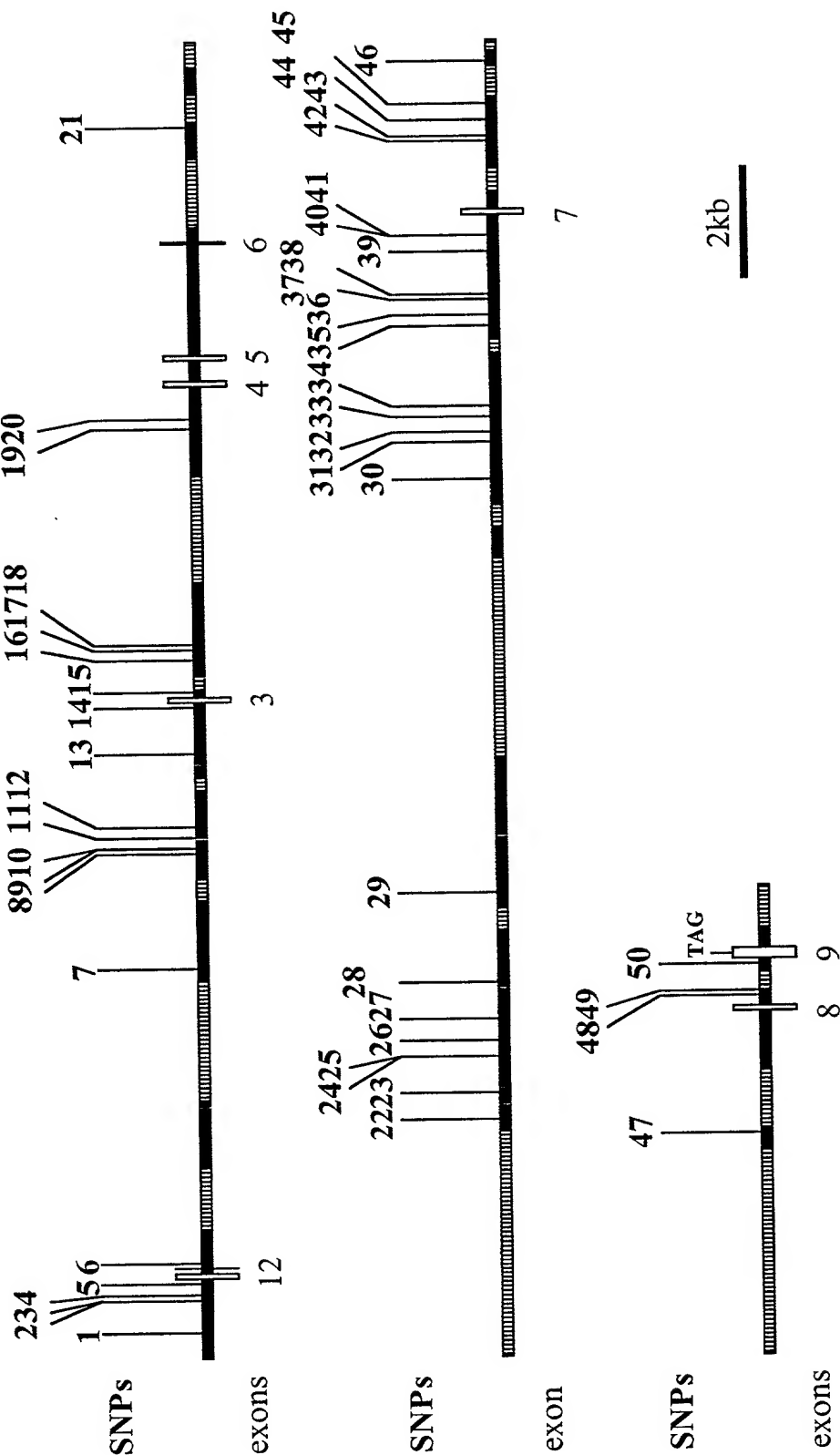
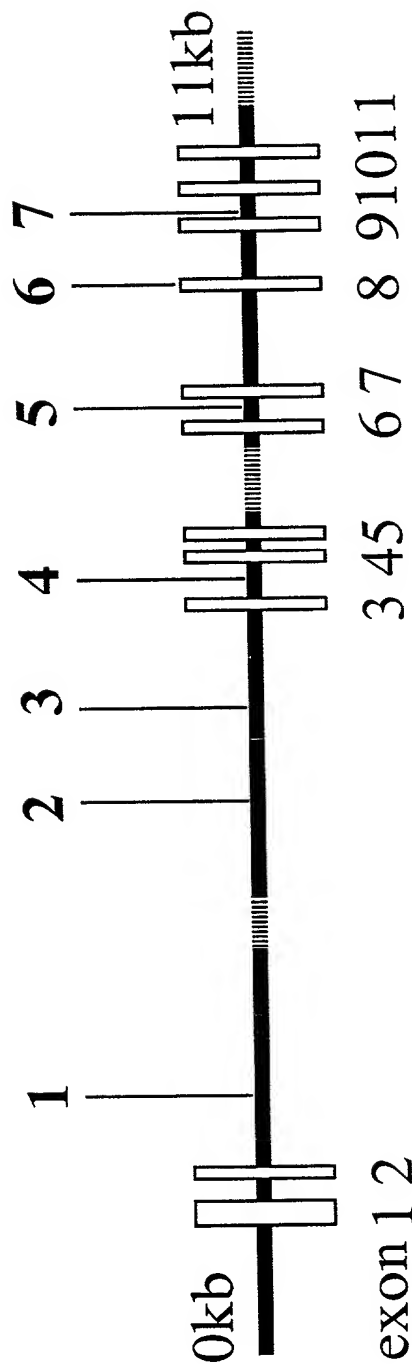


Fig. 300 *dolichyl-diphosphooligosaccharide-protein
glycosyltransferase (DDOST)*

Accession No. D89060



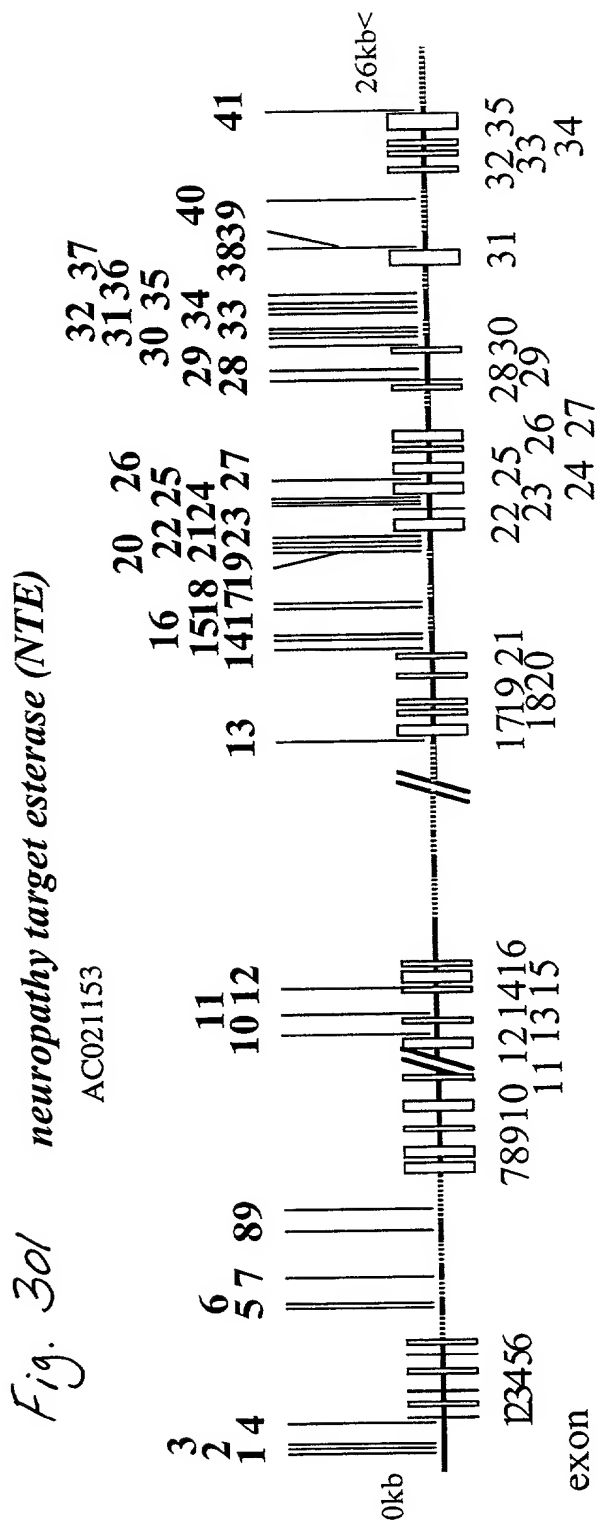


Fig. 302

L1 cell adhesion molecule (L1CAM)

Accession No. U52112

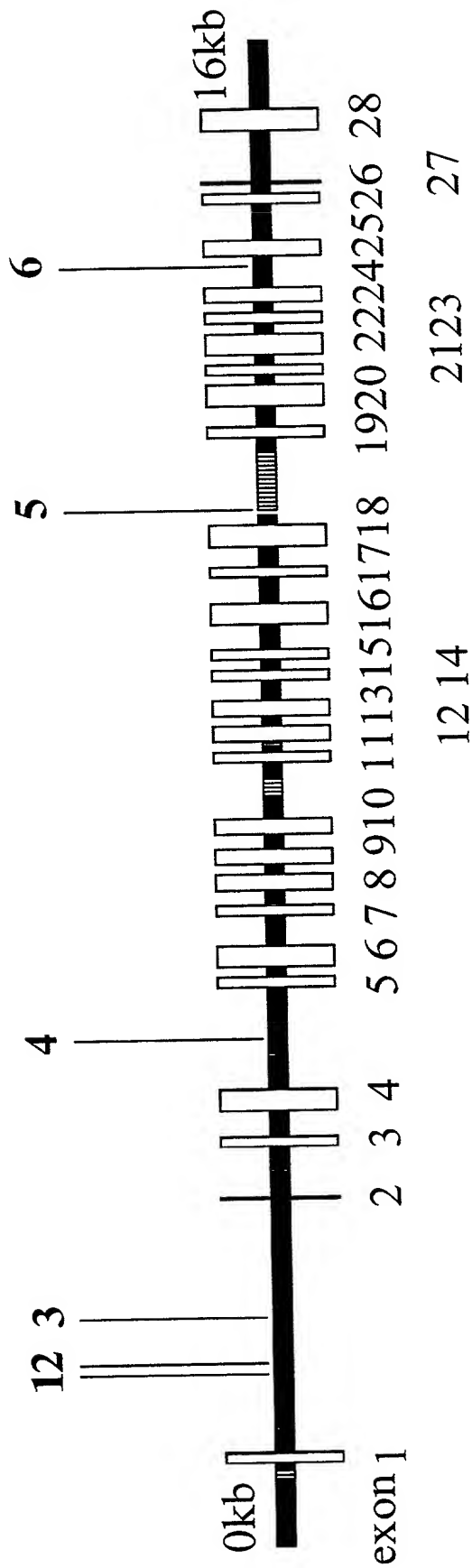


Fig. 303

arylalkylamine N-acetyltransferase(AANAT)

Accession No. U40391

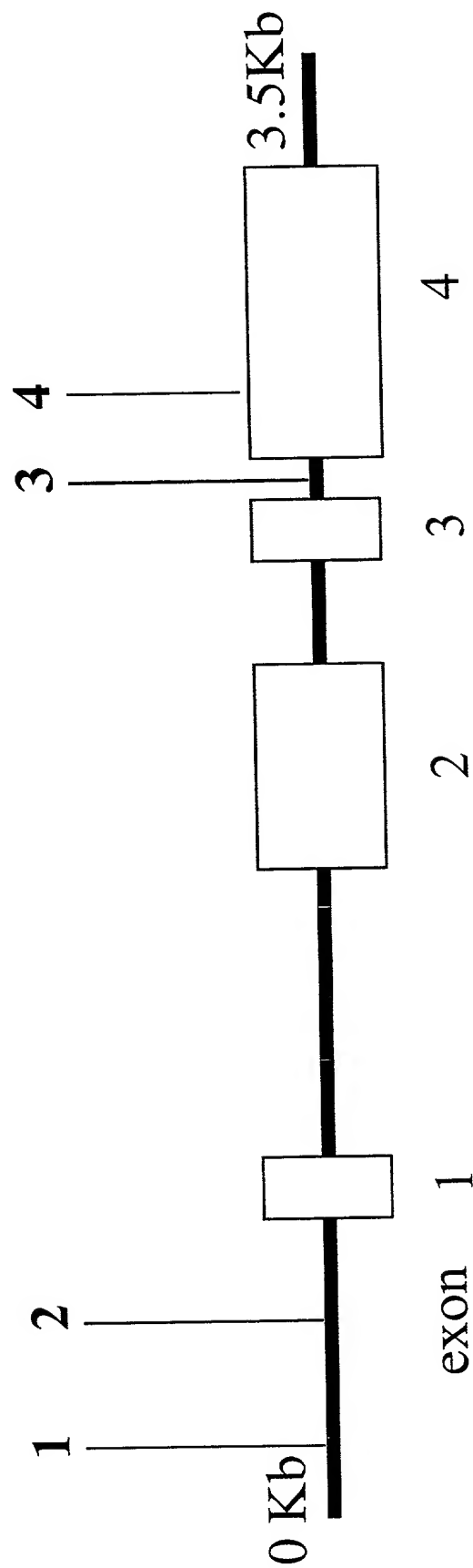


Fig. 304

N-acetyltransferase, homolog of *S. cerevisiae* (*ARD1*)

Accession No. U52112

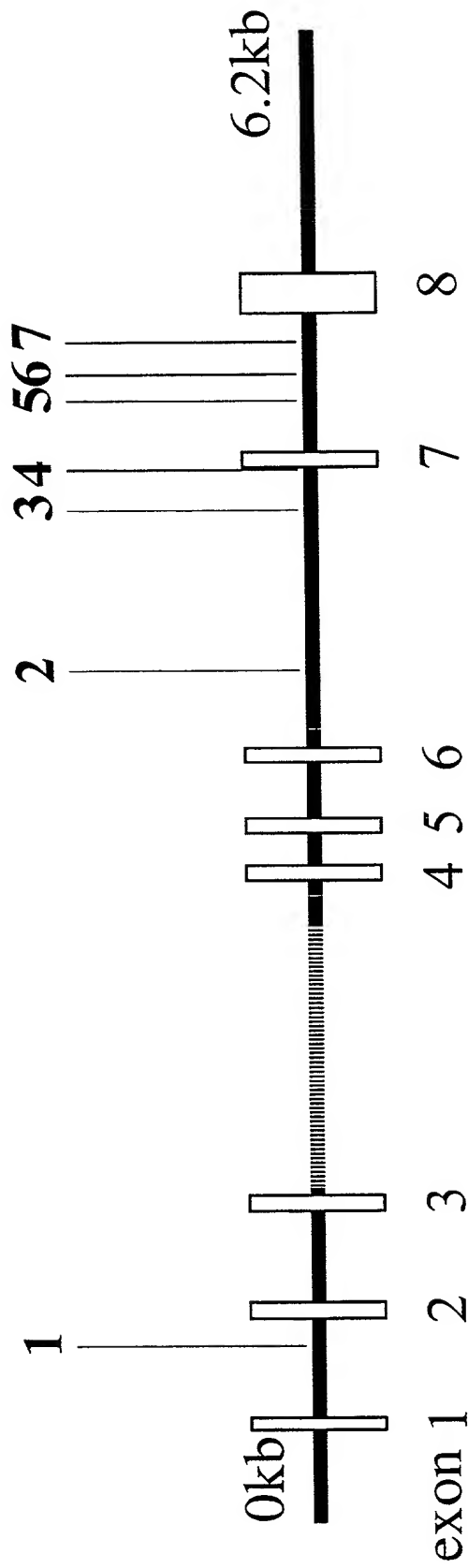


Fig. 305

N-acetyltransferase (NAT1)

Accession No. X17059

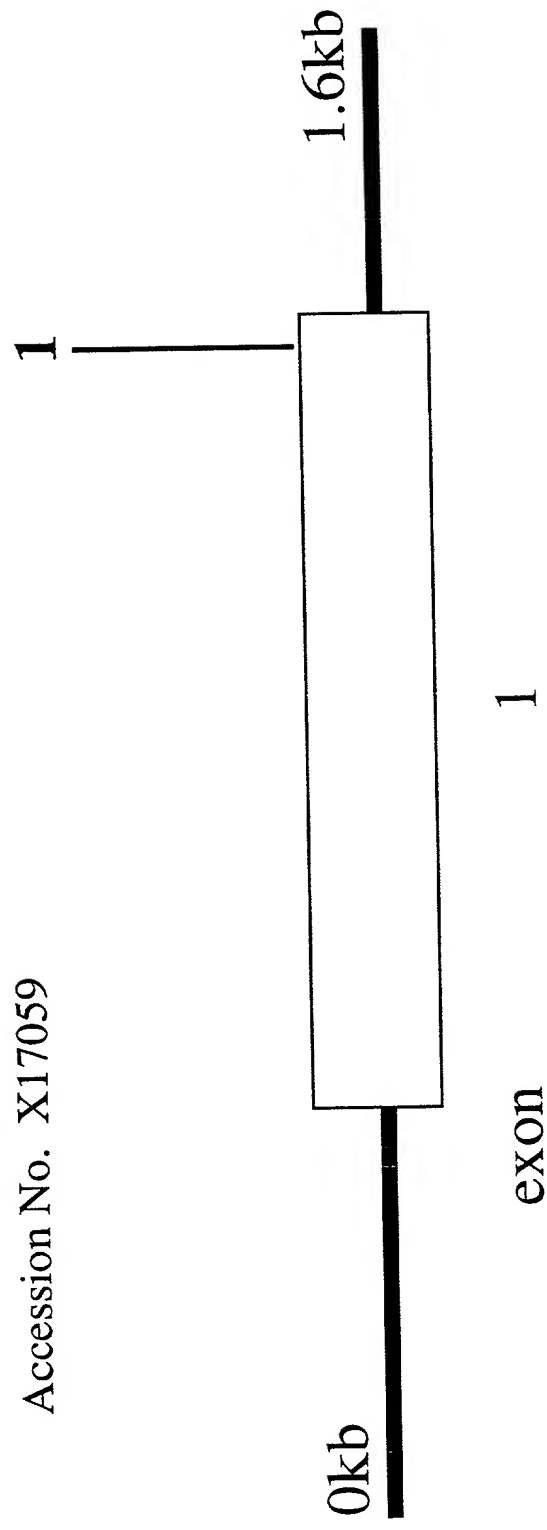


Fig. 306

N-acetyltransferase2 (NAT2) Accession No. D10870

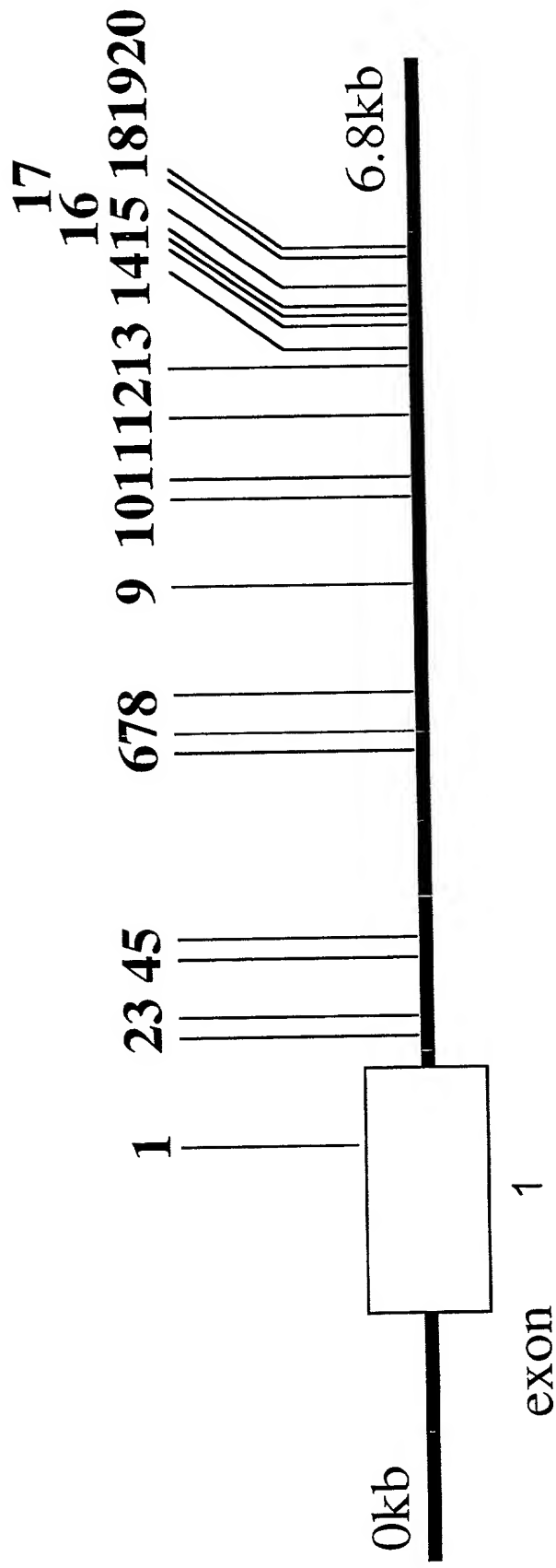


Fig. 307

ATP binding cassette, sub-family B, member 2 (ABCB2)

ACCESSION X66401

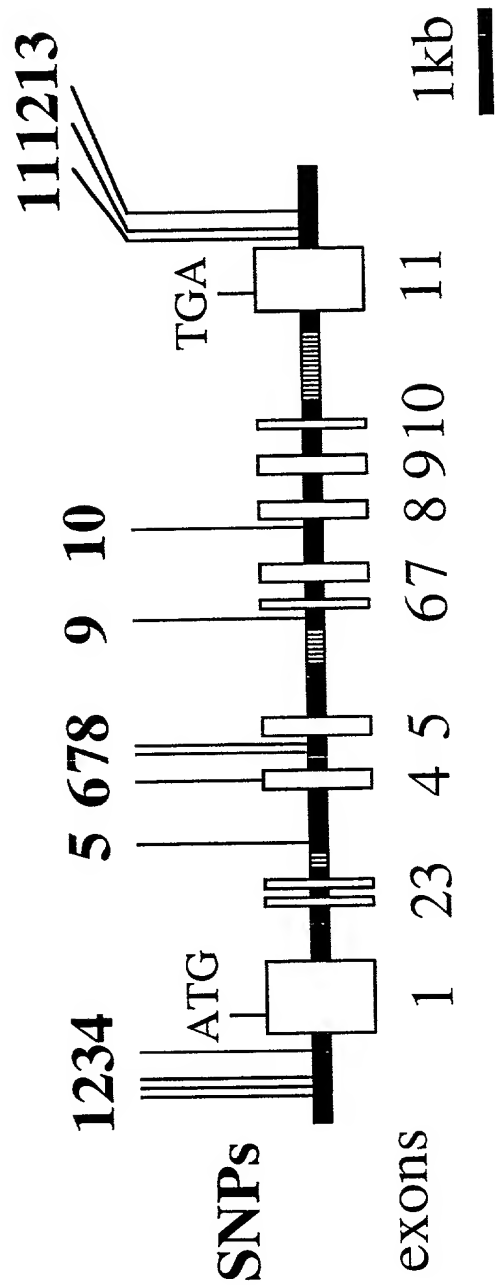


Fig. 308

ATP-binding cassette, sub-family B, member 3 (ABCB3)

ACCESSION X66401

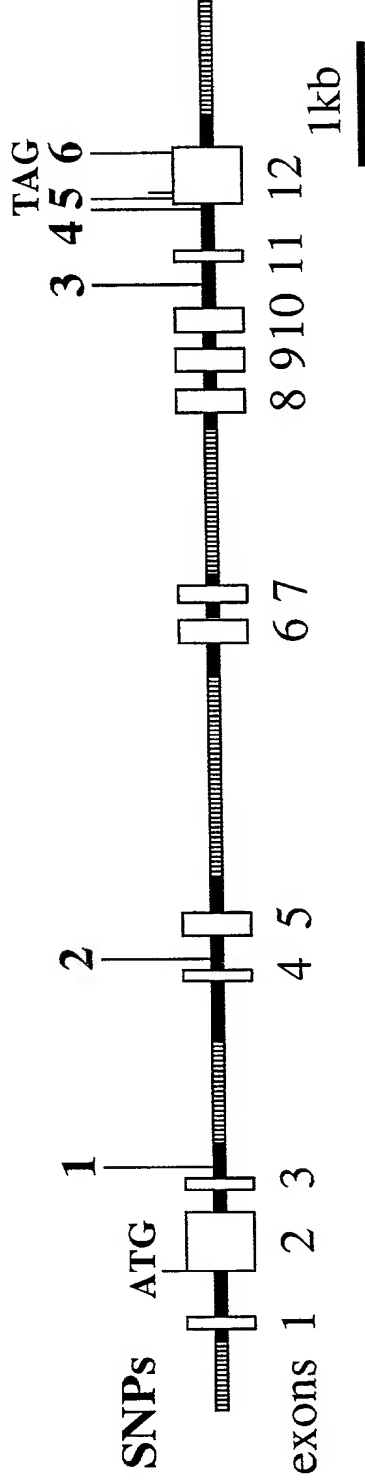


Fig. 309
Glutathione S transferase M3 (*GSTM3*): AF043105.1

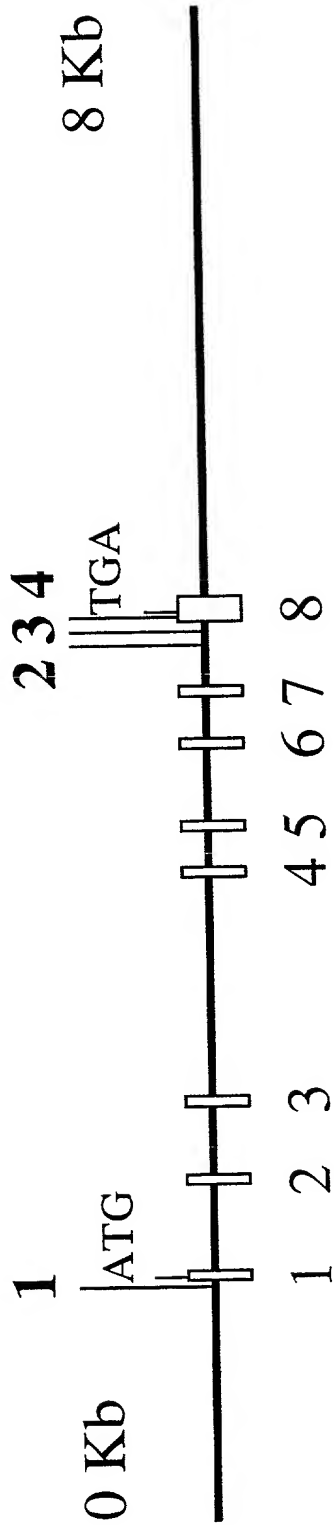


Fig. 3/0

Glutathione S transferase M4 (*GSTM4*): M96233.1

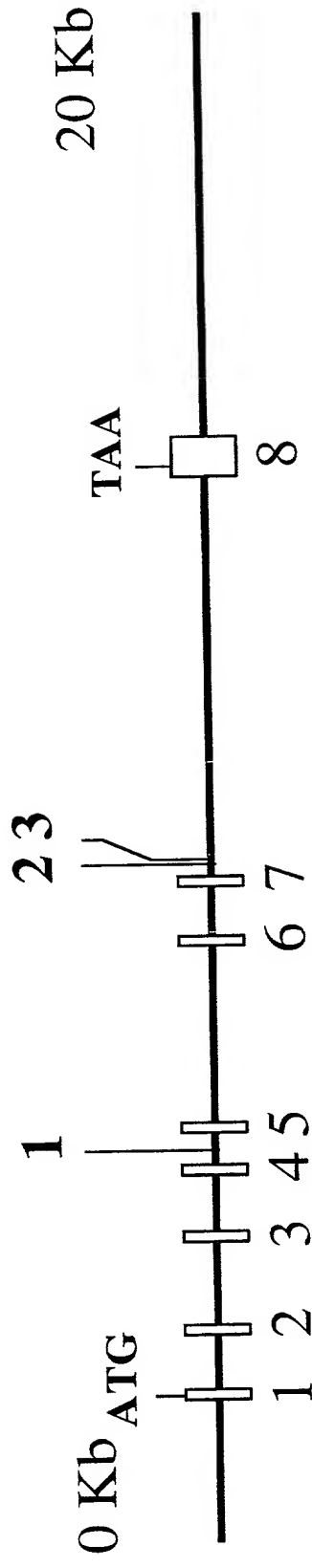


Fig. 3//

Aldehyde dehydrogenase 7 (*ALDH7*)

ACCESSION AC004923

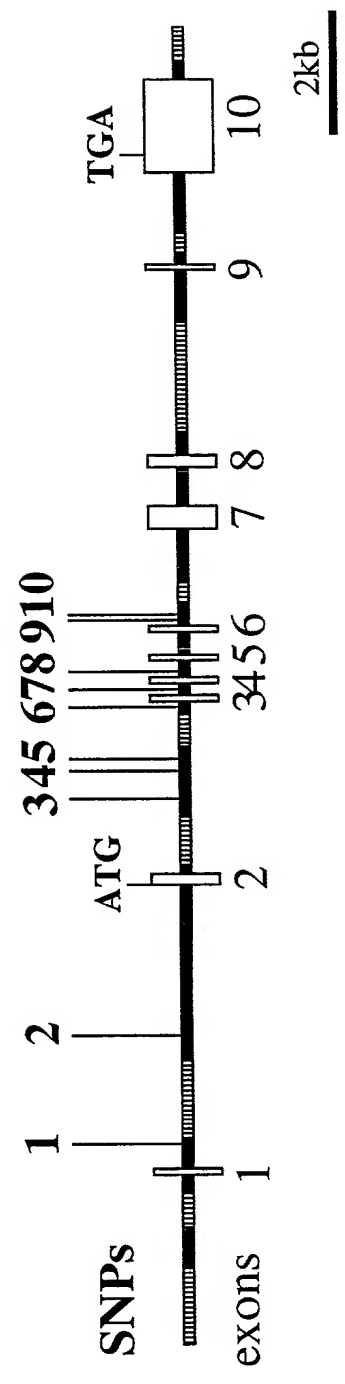
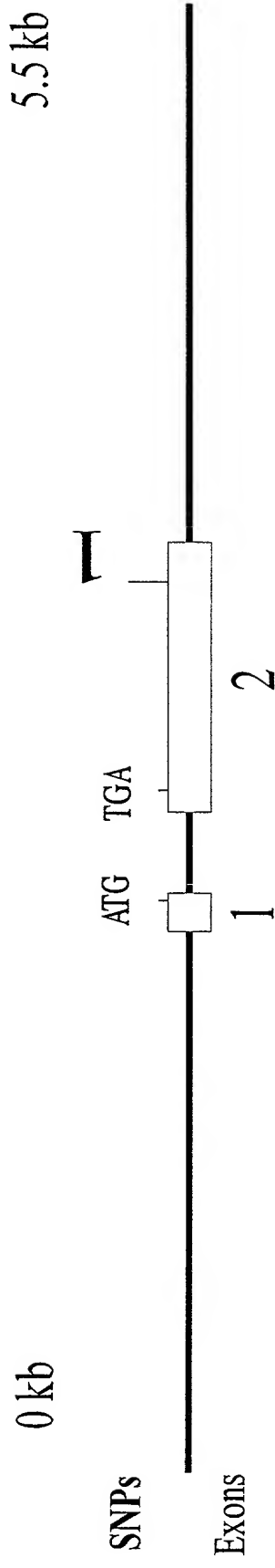


Fig. 3/2

High-mobility group protein 17-like 1 (*HMG17L1*)



SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST105177

General Information

JSNP ID : IMS-JST105177
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1184379	9	99064055

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CAGCCCCGAG CCCAGCGCTT CCCGCGCGTC TTAGCGCGGC GGGCCCGGC GGGGGAAGGG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105177

12/17/2001

TCCTTTCCTT

Observed : G/C
 3' Assay : ACGCAGACCG CGGACCCCTAA GACACCTGCT GTACCCTCCA CCCCCACCCC ACCCCACCCA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 1176 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_1
 Amplified region : 276..1402 in AF275948
 size : 1127

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TTCTACGGGT CTGTCCTGAG	
BackwardPrimer	:	AGAGTTACT ATCGGTCAA	G



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105177

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105183

General Information

JSNP ID : IMS-JST105183
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : ACCTCCTTTA AGACCCGATT TAATGCGCTC CCTCCTCATG AAGCTCTTCT GGATCCACTC
 Observed : T/C
 3' Assay : TTCCCATCAC TAAGTTGAAA GTAAGATCCC CTTCTCTTTA CTTCCATTAG ACTTGGATTA
 Comment :
 Sample size : 96

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105183

12/17/2001

TOGETHER

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 7636 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1.20000717_3
 Amplified region size : 7409..8565 in AF275948
 : 1157

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TCAGTTACTC TCCATTCTAC	G
BackwardPrimer	:	TTTGCATCTA TACTCCAGA	TG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105185

General Information

JSNP ID : IMS-JST105185
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1196308	9	99052126

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TCCAGGCCTC TTCATACTAT ACCAGAAATT AGGATAACTA TTACAGTGCC CTTTATAGGA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105185

12/17/2001

Observed : G/A
3' Assay : AGAAGAAGA AATTGTGTCT GTAGATGTCT GTTCCTTCA GCTTAAATG GACACTGAAA
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 13090 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_4
Amplified region : 12939..14128 in AF275948
size : 1190

Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCCATTACCC ACAGTGGTAG
BackwardPrimer : AATCCACTTA CTTGTGATTC TG

SNP Information for IMS-JST105189

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST105189
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1197894	9	99050540

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : AAGTGCCCT TGCTTGATGG CATGTTTACC AGGGTTCTA GAGCCTCAAT CACAGATTCT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105189

12/17/2001

Observed : C/G
3' Assay : TCTAGCTCAC ATGAAGTTAA TGAAATGAA TGTGCTTCCC TACAAATTAG AGAGGCTTTG
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 14676 ([View SNP position in this record](#))

Method

PCR Method
[Sequence Method](#)

PCR Profile

Screening region ID : AF275948.1_20000717_5
Amplified region : 13772..14995 in AF275948
size : 1224

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	ATGTTAAACAC TTAGCGGTT G	
BackwardPrimer	:	GCAATGTGCA ACAAGCTACT G	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105189

12/17/2001



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



SNP Information for IMS-JST105191

General Information

JSNP ID : IMS-JST105191
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1203657	9	99044777

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GGAGACTTCC CTCCTCTGGA ACCTGCCCTG GCTCAGGCAT GAGGGCTGAC TGTACCCCTT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105191

12/17/2001

Observed	:	T/C
3' Assay	:	GATAGAGCC CAGCACTAA GCTCATGTGT TGGCAGTGT CTTCGGGAA GGAAGAAGAC
Comment	:	
Sample size	:	96

```

Accession No.      : AF275948.1 (Graphical View of this Entry)
Chromosome         :
map               :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in sequence  : 19522 (View SNP position in this record)

```

PCR Method
Sequence Method

Screening region ID	:	AF275948.1.20000717_6	
Amplified region	:	19125...20141	in AF275948
size	:	1017	
Pre-Denature	:	94.0 degrees	C for 2.00 minutes
Denaturation	:	94.0 degrees	C for 0.50 minutes
Annealing	:	60.0 degrees	C for 0.50 minutes
Polymerization	:	72.0 degrees	C for 2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees	C for 7.00 minutes
ForwardPrimer	:	GGATAGAACT	CTGAGAAATG C
BackwardPrimer	:	CAATGAACCTG	AGAGACTGGA C

12/17/2001

[illegible]

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105191

SNP Information for IMS-JST105199

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105199
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Keyword

[Search](#)

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Allele Sequence

Variation Type : SNP

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105199

12/17/2001

Flanking Sequence Information

5' Assay : CTTCCTGATT TCTAAAGGAA GTATATTTTG CTGAATCAGA AAGAAAAGTG ATTTATTTC
Observed : A/G
3' Assay : GTTGCTCATG CTTAGATTCT TAGAGTTGCA AAGATCTGGC TTGCAATCTTG TACAACTGAC
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 28790 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_11
Amplified region : 28480..29670 in AF275948
size : 1191
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

SNP Information for IMS-JST105202

General Information

JSNP ID : IMS-JST105202
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Allele Sequence

Variation Type : SNP

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105202

12/17/2001

Flanking Sequence Information

5' Assay : CAGCCCTGCC CATTAGGTAG GGAAGAAGT TAGCAGTCCA TGATAGCTGT TGCCTGCAGC
Observed : A/G
3' Assay : TACGGAGGTT CATTGGCAG TTCCTGTCTC CTGAGATCCT GGAGTGTATA CGCTTGGCCT
Comment : repeat sequence (repeat sequence exists in flanking sequence)
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 29176 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_11
Amplified region : 28480..29670 in AF275948
size : 1191

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes

Forward Primer

ForwardPrimer : GAATCCTGCA ACAGGATGTG
BackwardPrimer : ACACAAGTTA ACTGTTACTT TG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105202

12/17/2001

SNP Information for IMS-JST105205

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105205
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Allele Sequence

Variation Type : SNP

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105205

12/17/2001

Flanking Sequence Information

Flanking Sequence	Information
5', Assay	: TAGGGGAAGA AGTTAGCAGT CCATGATACC TGTTGCCTGC AGCATACGGA CGTTCATTGC
Observed	: G/A
3', Assay	: CAGTTCCTGT CTCCTCAGAT CCTGGAGTCT ATACGCTTGG COTCAGAGCC CAGCAGACAG
Comment	: repeat sequence (repeat sequence exists in flanking sequence)
Sample size	: 96

```

Accession No.      : AF275948.1 (Graphical View of this Entry)
Chromosome         :
map               :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence  : 29193 (View SNP position in this record)

```

PCR Method
Sequence Method

```

Screening region ID : AF275948.1.20000717_11
Amplified region   : 28480..29670 in AF275948
size                : 1191

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes
Annealing          : 60.0 degrees C for 0.50 minutes
Polymerization     : 72.0 degrees C for 2.00 minutes
PCR Cycles         : 35
Post-Extension     : 72.0 degrees C for 7.00 minutes

```

Sequence

ForwardPrimer : GAATCCTGCA ACAGGATGTG
BackwardPrimer : ACACAAGTA ACTGTTACTT TG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105205

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105206

General Information

JSNP ID : IMS-JST105206
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1213528	9	99034906

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CTTGAGGAGG CTCCCTTGCA CTAGGAAGAA TAGAAGCAT ACATAAGCC TGTGTGCTGC
 Observed : T/C
 3' Assay : GCCAGGAAGA CTAGAAACGC TATGTTTCAGC CTGGAGCTGA ATGTTATACC CCAGAGCAAC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 29390 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1.20000717_11
 Amplified region : 28480..29670 in AF275948
 size : 1191
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

FOOTNOTES

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : GAATCCTGCA ACAGGATGTG
BackwardPrimer : ACACAAGTGA ACTGTTACTT TG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105206

SNP Information for IMS-JST105207

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST105207
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1224077	9	99024357

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TTAGCACAGC AGGTTGGCCT GGTCTCTCTCC TCTCAACATA GTCACCACAT ACCTGGCACT
 Observed : A/G
 3' Assay : TCCTAAGGCT GGAATGCCAG ACAGATGGGT GCCTGCTTTC AGAGTGCTCA ATGTGCTGAG
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 39916 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_12
 Amplified region size : 39854..40990 in AF275948
 : 1137
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

PCR "CCTT" "CCTTCTT"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : ATTTAGCACA GCAGTTGGC
BackwardPrimer : TATGCTCACT GTAAAGGCTG T



12/17/2001

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SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST105217

General Information

JSNP ID : IMS-JST105217
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1236608	9	99011826

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105217

12/17/2001

TCAGT "CCCCCT

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TAATAATGAT GACAGAAGTT CTTCAAAAAG TCTTGGCCTT CTTCTTTCA CAAAATTGCC
 Observed : C/T
 3' Assay : CCCAGACCTT TCTGGAAGGG CAGCCATGAA CCAGAGAGGCC TAAAGTAGAT TTAAGTGGAA
 Comment : repeat sequence (repeat sequence exists in flanking sequence)
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 52465 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_17
 Amplified region : 51992..53206 in AF275948
 size : 1215
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

PCR "CONDITION"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGTTCCTGGC TGA CTGTTG
BackwardPrimer : ACTATGAGCC AAGTAGGACG



12/17/2001

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SNP Information



[SNP Home](#)

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105218

General Information

JSNP ID : IMS-JST105218
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1237515	9	99010919

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

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12/17/2001

PCR "REPEAT"

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AGGCATACAG	TGAGGGAAC
BackwardPrimer	:	CAAGAGCTAC	ACTGGACAC



PCR "E3E00"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TTGTTGCTGC TCAGAAATCAT G
BackwardPrimer : AAGGTGATAT GTCCTCCAAA G



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105218

SNP Information for IMS-JST105219

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105219
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1243362	9	99005072

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

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12/17/2001

TOP "CE33600"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CCAGTCTGA CTGATTCTGG AGTGGCAGAG AGGTTGGAG GGTACCGCT CTGCTCACCC
Observed : G/C
3' Assay : ACCCTCTGGC CATCTCCTCT TAGAATGCAA GGCAGGGAT TTTGTTACAC AGCGCCTCTT
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 59219 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_19
Amplified region : 59130..60334 in AF275948
size : 1205
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

PCR "SCREENING"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : ATGAGTAATG TCTCGTTCCA C
BackwardPrimer : ATCACATCAG CATCCCAGGC



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105219

SNP Information



[SNP Home](#)

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



SNP Information for IMS-JST105225

General Information

JSTP ID : IMS-JST105225
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1249738	9	98998696

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

AF275948.1

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : AAGTAAACA ATGTTCTTAA AACTGTGGTT CCACACCTCC CTCCCCAAC ATTAAAAGTG
Observed : T/C
3' Assay : AAGGGATGCT TATTCAAATG TAGATTGTGA GGCTCTGCAC TCTAGACCCA CTATTTCAGA
Comment : repeat sequence (SNP is present in repeat sequence)
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 65594 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_22
Amplified region : 65150..66351 in AF275948
size : 1202
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

PCR Condition

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TTCACACCAG TCCTCAACTG
BackwardPrimer : GCCCTATGAC TCGGAAACAG



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12/17/2001

SNP Information for IMS-JST105229

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105229
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1250219	9	98998215

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

12/17/2001

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Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ACTGGCTGGG CTGTCAGGCC CTCCTGTTAC TTATCTCTG CATGTGACCC TCTTAGCTCC
Observed : G/A
3' Assay : CGGATTAACT CCTGTCTCTCA TTAAGCCTCA CACTGTAGCC CCATTTTCAG ATCAAACTG
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 66075 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1.20000717.22
Amplified region : 65150..66351 in AF275948
size : 1202
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TTCACACCAG TCCTCAACTG
BackwardPrimer : GCCCTATGAC TCCGAAACAG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105229

SNP Information for IMS-JST105238

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105238
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1255690	9	98992744

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

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12/17/2001

TOGETHER

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : ATTGTGGGCT GTACAGTTG GAAGGCCCTG GAATTAGATG AGACCACACT ATTTAGCTTA
 Observed : C/T
 3' Assay : TTAGTAATAA CATTGCAAG AAAAATTCCG ACGAAGTTTT TTCAGCCTAG GAATCAATAG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCAL (ABCA1) gene, complete cds.
 Position in Sequence : 71478 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_25
 Amplified region : 70681..71942 in AF275948
 size : 1262
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105238

12/17/2001

PCR "E3E00T"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : AGACCTGATG CATTGGACTG
BackwardPrimer : AAGTCACAT TCTAGGGTAT G



PCR Condition

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGTCAGGAAG CAGCAGTGAT
BackwardPrimer : ACATTGCAG ATATCAGCTA C



TCCTTCTG CCCCTCTGCT

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TTGTGGATGC GTTGGTTTAT GACCAGGTAT TGATTAAGGT GGCTACTACC
 Observed : A/G
 3' Assay : GGTGCTTTCT GCATATCTCG GGTTTGTGGA GCACTCAGGT TCTGCTTCTG CCCCTCTGCT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 73129 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_26
 Amplified region : 72579..73742 in AF275948
 size : 1164
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

PCR Cycle Sequence

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : AGTTAGAGAA GCTGACTTGT G
BackwardPrimer : ACTGCCATAC TTCCCATG



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12/17/2001

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword



General Information

JSNP ID : IMS-JST105261
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1275854	9	98972580

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

[illegible]

Screened Sequence

Method

PCR Profile

```

Screening region ID : AF275948.1_20000717_35
Amplified region   : 91500..92700 in AF275948
size                : 1201

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes
Annealing          : 60.0 degrees C for 0.50 minutes

```

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105261

12/17/2001

THE "SECRET" DATABASE

SNP Information for IMS-JST075566

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075566
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403406	4	68103408

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TCACCTTTGC CTCATACAGG TAAATCTAAG AAAGTAGGGA CTATGAGAAC CCCATATGTAT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075566

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105263

General Information

JSNP ID : IMS-JST105263
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1276632	9	98971802

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

TOP of the page

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GGAGGAGCCA AACGCTCATT GTCTGTGCTT CTCTCTCTTT TTCTGCGGTC CCTGGCTCCC
 Observed : C/T
 3' Assay : ACCTGACTCC AGGTGAACAA GACCTTCCAG GAACTGGGCTG TGTTCATGA TCTGGAAGGC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 92420 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_35
 Amplified region : 91500..92700 in AF275948
 size : 1201
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

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TOGETHER

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TTGCTTGAAA ACTGAGGTCT G
BackwardPrimer : GTGGTGCCCT GTGACTTTAG



12/17/2001

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SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword



SNP Information for IMS-JST105269

General Information

JSNP ID : IMS-JST105269
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1281507	9	98966927

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Top of the page

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TATCTCAGTG ACTAATGGTA GCAAGGCATT CCTTAAAAA GGCAATTATTT GTGAAACTTAA
Observed : T/C
3' Assay : CTAAATCGA ATTCCGGGTCC AATTAAATTT TTGAAATTTT ATATTAAAAA TTATATTAGT
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 97295 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_38
Amplified region : 96698..97787 in AF275948
size : 1090
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : GTAGTGCTCC TCAAGATTTA G
BackwardPrimer : AACTTCCTCT CATCCAGCAG



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12/17/2001

SNP Information for IMS-JST105273

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST105273
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1286207	9	98962227

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105273

12/17/2001

Top of the page

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ATCAAGAGGG AAGTCAAGT TGCCTGGCCA TTTTCCCTTGG CTTTAGACA GAAAAGTTAC
Observed : G/A
3' Assay : TGGGATATTA TCTCCACAG CTCCTCTGTG GTGCCACCAG TCATAGTCCT TATATAAGGA
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCAL (ABCAL) gene, complete cds.
Position in Sequence : 101995 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_40
Amplified region : 101849..102994 in AF275948
size : 1146
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

PCR "SEQUENCE"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CCTGCAGACA TGTACCCATC
BackwardPrimer : CAAGAGAGGT CATCTCTGAC



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105273

SNP Information for IMS-JST105285

SNP Information



SNP Home

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[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST105285
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1293242	9	98955192

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron *1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105285

12/17/2001

[illegible]

Sample size : 96

AF275948.1 (Graphical View of this Entry)

109030 (View SNP position in this record)

PCR Method
Sequence Method

```
Screening region ID : AF275948.1_20000717_44
Amplified region   : 108579..109721 in AF275948
size               : 1143
```

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105285

12/17/2001

--- SNP INFORMATION ---

Forward primer sequence

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CTTTGAATAT GGCAGGCTCA C
BackwardPrimer : CAAGTTCTG TTACCAACCG C



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105285

12/17/2001

SNP Information for IMS-JST105289

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



General Information

JSNP ID : IMS-JST105289
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1295180	9	98953254

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105289

TOP SECRET

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CAGCCAGGAC TTGCTGGCTG TGAATGATTT CTCCATCTCC ACCCCTTTTG CCAIGTTGAA
 Observed : A/G
 3' Assay : CCACCATCTC CCTGCTCTGT TGCCCTTTG AAATCATATC ATACTTAAGG CATGGAAGC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 110968 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_46
 Amplified region : 110159..111199 in AF275948
 size : 1041
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

PCR "E3E00T"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GGTTAGTTGA AAGGTGGAT G
BackwardPrimer : ATGAGCAGGA ACACCAGGTC



SNP Information for IMS-JST105294

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105294
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1299776	9	98948658

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105294

12/17/2001

AF275948.1

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AAGTGATAG ATCCCTACAG AGTCCAAAGA GAAGTGAGGA AATGGTAAAA GCCACTGTGT
 Observed : C/T
 3' Assay : TTTCAGCAT CGTGATGTG ATCAAACCTG AAAGAGCCTA TCCATATCAC TTCCTTTAAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 115563 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_49
 Amplified region : 114846..115694 in AF275948
 size : 849
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

PCR Conditions

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGATAGCTCT CACCACTGAG
BackwardPrimer : AAGAACTAG GACCCGCGAG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105294

12/17/2001

FILED "0003000"

SNP Information for IMS-JST105296

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105296
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1302524	9	98945910

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

TOGETHER

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GCCCAATGTA GTCTTTCTCA GTCTTCAGGA GGAGGAAGGG CAGGACCCAG TGTTCAGT
Observed : C/T
3' Assay : ACCCTGAATG TGAGCACTAT TTACTTCGTG AACTTCTTGG CTTAGTGCCT CTGCCAGGTG
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 118311 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_50
Amplified region : 117331..118503 in AF275948
size : 1173
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

PCR REACTION

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCAGCTGTCA TAACATGAGA G
BackwardPrimer : GACCAACCAG CACGGCAATG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105296

SNP Information for IMS-JST105297

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105297
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1304647	9	98943787

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105297

12/17/2001

Top of Page

Allele Sequence

Variation Type : SNP
Flanking Sequence : Information
5' Assay : CCCAGCCCCT GTACTTAAGT GCTTCAATAG GCTCTCAATTA TATATGATTT TTAGGTTTTG
Observed : T/C
3' Assay : TTATCAGCCTT CTTCGCTTTT ATAATCTGAA AAGATGGCAT ATGAATTTTT ATAAAAAGGG
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 120434 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_51
Amplified region : 120141..121315 in AF275948
size : 1175
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

PCR "EFFECT"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TGCATGCCAC ATTGTACCG
BackwardPrimer : GGGCTCAGAC ATCATGTTTG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105297

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105299

General Information

JSNP ID : IMS-JST105299
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HCBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1305308	9	98943126

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-JST105299

12/17/2001

Allele Sequence

Variation Type	: SNP
Flanking Sequence	: Information
5' Assay	: CCAGATGACA AGGATAGAGA AGGCACAGA CACGGCCTAT CTGGATTCA TGGTGCCITTT
Observed	: G/C
3' Assay	: ATTTTCACA TGAAGTTGT GTAGGGAAGA TAGAACCATG AGATCAGATG ATAAATAGT
Comment	: repeat sequence (SNP is present in repeat sequence)
Sample size	: 96

Screened Sequence

Accession No.	:	AF275948.1	(Graphical View of this Entry)
Chromosome	:		
map	:		
Definition of the record	:		Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence	:	121095	(View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

```

Screening region ID : AF275948.1_20000717_51
Amplified region   : 120141..121315 in AF275948
size               : 1175

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes
Annealing          : 60.0 degrees C for 0.50 minutes

```

PCR "E3E00"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGCATGCCAC ATTGTGACCG
BackwardPrimer : GGGCTCAGAC ATCATGTTTG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105299

12/17/2001

SNP Information for IMS-JST105301

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105301
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1311083	9	98937351

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

AF275948.1

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AAAATCAGAT AGGTGATGTG GCTACGTCAG GGGGCCGAA GGCTCCTTGT TACTGATTC
 Observed : C/T
 3' Assay : GTCTTTTCTC TCTGCCTTTT CCCCAAGGC CAGGACCCCT GGATCTCTGG GCAGAGCAGA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 126866 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_53
 Amplified region : 126539..127601 in AF275948
 size : 1063
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

PCR # CCGGCGT

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGCAGGTGTC TAGGGATTTC
BackwardPrimer : CCAAGACGG CTCTGTATGC



SNP Information for IMS-JST105304

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105304
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1311346	9	98937088

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105304

12/17/2001

TGAGGTTTGGGAGTTT

Allele Sequence

Variation Type : SNP
 Flanking Sequence : Information
 5' Assay : CCACTGGGTT GGAGGAGCAT CTGTGAGATG AAACACCAATT CTTTCCTCAA TGTCACAGCT
 Observed : A/G
 3' Assay : TCTAACTGTG TGTGTAATCA GGCCAGGTCC TCCCTGTCTGG GCAGAAACCA TGGGAGTTAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 127129 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_53
 Amplified region : 126539..127601 in AF275948
 size : 1063
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

T024T"EE3600T

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGCAGGTGTC TAGGGATTTC
BackwardPrimer : CCAAGACGG CTCTGTATGC



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105304

12/17/2001

SNP Information for IMS-JST105312

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105312
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1319606	9	98928828

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

AF275948.1

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GTGTCCTCTGA TAGCATTGAG ARAAGTGAAA GGCAGTTTT GAAGGTAAGG AAAATAGTGT
Observed : T/C
3' Assay : ATTTGCTTGG ATCCACTGGC TCATGCCACT GTCCTGGTTG GTTAGAAGCA CTGGAAAAAGT
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 ([Graphical View of this Entry](#))
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 134901 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_58
Amplified region : 134281..135220 in AF275948
size : 940
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes

--- SNP INFORMATION ---

Sequence "E6E6E600T"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : ATACTCAG CATTCTCCA G
BackwardPrimer : AGCCCTCTT CTATGAACAG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105312

SNP Information for IMS-JST105319

SNP Information



SNP Home

Search

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BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105319
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1321488	9	98926946

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105319

12/17/2001

Allele Sequence

Variation Type	:	SNP
Flanking Sequence	:	Information
5' Assay	:	TTAATTTTTA AAATACCTGC AATACATATA TATCTTGAAT AGATGAAAAA TTATGTAGAT
Observed	:	G/A
3' Assay	:	ATAATGAATG ATACGTTCT AAAAAGACAG GTTAAAAAGT AAGTTCACCTT TTATTTTGAG
Comment	:	
Sample size	:	96

Screened Sequence

Accession No.	:	AF275948.1	(Graphical View of this Entry)
Chromosome	:		
map	:		
Definition of the record	:	Homo sapiens ABCA1 (ABCA1) gene, complete cds.	
Position in Sequence	:	136783 (View SNP position in this record)	

Method

PCR Method
Sequence Method

PCR Profile

```

Screening region ID : AF275948.1_20000717_61
Amplified region   : 136633..137272 in AF275948
size                : 640

Pre-Denature       : 94.0 degrees C for 2.00 minutes
Denaturation       : 94.0 degrees C for 0.50 minutes
Annealing          : 60.0 degrees C for 0.50 minutes

```

PCR "CCT" 6600

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CCTCTAGATG CCAGCATCTC
BackwardPrimer : ATTCTCTTGA CATAAGGGT C



SNP Information for IMS-JST105320

SNP Information



SNP Home

Search

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FTP Server

Search Example

General Information

JSNP ID : IMS-JST105320
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1321501	9	98926933

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TACCTGCAAT ACAATATAT GTTGAATAGA TCAAAAATTA TCTAGATGAT AATGAATGAT
 Observed : A/G
 3' Assay : CGGTTCTAAA AAGACAGGTT AAAAAGTAAG TTCACCTTTTA TTTTGAGCTT CAGAATCATT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 136796 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_61
 Amplified region : 136633..137272 in AF275948
 Size : 640
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

Table 1

Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCTCTAGATG CCAGCATCTC	
BackwardPrimer	:	ATTCTCTTGA CATACAGGT C	



THE "GENE" PROJECT

SNP Information for IMS-JST105324

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105324
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. (in press)
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1323098	9	98925336

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105324

12/17/2001

TCCTGCT " CCGGCGCT

Allele Sequence

Variation Type : SNP
 Flanking Sequence : Information
 5' Assay : AGCTTTATTC AGGTATAATT TACATACAAAT ATAATTGCT TGTTTTAA GAGTATAATT
 Observed : T/C
 3' Assay : AGTGATTTT GGTAATTGA GAGTTTGA ACCATCACCA CAATCCAGTT TTAGAACTTT
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 138393 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1.20000717_62
 Amplified region : 137780..138813 in AF275948
 size : 1034
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

12/17/2001

Experiment "E63E007"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CTTGGCCTC AACTTGACAA C
BackwardPrimer : AAATGGCCTA ACGGTGGCTC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST105327

General Information

JSNP ID : IMS-JST105327
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1324484	9	98923950

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
AF275948.1	genomic	ABCA1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105327

12/17/2001

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GCAGTAATAA CCAGCCCATTA GTAAGTTTG TCACAGGGAC TGGTTGTAAG AACTGATTTG
 Observed : G/A
 3' Assay : TTGGTATAGC TGTGAGGGCC TGGCAGGGTG TCCACGTGTG CCTCAATCCT AATTCTGAAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 139779 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_63
 Amplified region : 138622..139911 in AF275948
 size : 1290
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes
 Annealing : 60.0 degrees C for 0.50 minutes

PCR Cycle "E3E00T"

Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CCCCTATGT ACATGTACCT
BackwardPrimer : GCCATGAAC TGGCCTTCTG



SNP Information



SNP Information for IMS-JST105335

General Information

SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

JSNP ID : IMS-JST105335
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HCBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1331322	9	98917112

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TTGTTTGGG AAGTTCAAGT GATCTTCAA TATCATTAAT AACTTCTTCC ACTTTTCCA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105335

12/17/2001

Observed : G/A
3' Assay : AATTGGAATA TTAACGCTAA AGGTCTAAGA CTTCAGATT CAAATTAATC TTCTATATT
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
Chromosome :
map :
Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
Position in Sequence : 146617 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_68
Amplified region : 146071..147232 in AF275948
size : 1162

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTCTCAGTAC ACTTCCTGTG	
BackwardPrimer	:	CATAGGTACA TTCCACAGGG A	

Footnote



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105335

12/17/2001

SNP Information for IMS-JST105336



General Information

JSNP ID : IMS-JST105336

dbSNP ID(rs#)

Organism : Homo sapiens

Molecular type : Genomic

Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. (in press)

Release Date : 2001/08/09

Last Update : 2001/08/09

Keyword

Source: Author's calculations.

search

NEW Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008470.5	1331337	9	98917097

Gene Information

Allele Sequence

Variation Type : SNP

Flanking Sequence Information

5' Assay : CAAGTGATCT TTCAATATCA TTACTAACTT CTCACACTTT TTCCAGAATT TGAATATTA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105336

12/17/2001

TCCTTCTTCT ATATTTTAA AATTACAGA

Observed : C/T
 3' Assay : GCTAAAGGTG TAAGACTTCA GATTTCAAAT TAATCTTCT ATATTTTAA AATTACAGA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : AF275948.1 (Graphical View of this Entry)
 Chromosome :
 map :
 Definition of the record : Homo sapiens ABCA1 (ABCA1) gene, complete cds.
 Position in Sequence : 146632 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF275948.1_20000717_68
 Amplified region : 146071..147232 in AF275948
 size : 1162

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes

ForwardPrimer : GTCTCAGTAC ACTTCCTGTG
 BackwardPrimer : CATAGGTACA TTCCACAGGG A

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105336

12/17/2001

TOGETHER



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105336

12/17/2001

SNP Information

SNP Information for IMS-JST105354



General Information

SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

JST ID : IMS-JST105354
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

search

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022863.5	505008	4	97016801

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022863.3	genomic	ADH3	intron*1	Annotated	

NT 022863.3

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TCGAGAAGGG GTGACTACAG TCACACCAGG TACAGGATTC ACACTCAGGG AACATGCCTT
 Observed : G/A
 3' Assay : GTTCACCATC ACAAGATTAG TCAGCCTGGA TGAGGAACCC GAGGCAATGA AAGACGAAAG
 Comment : repeat sequence (repeat sequence exists in flanking sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_022863.3 ([Graphical View of this Entry](#))
 Chromosome : 4
 map
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 876996 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_022863.3 20010416 11
 Amplified region size : 876463..877418 in NT_022863
 : 956
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105354

12/17/2001

PCR Cycling

Annealing : 60.0 degrees C for 0.50 minutes
 Polymerization : 72.0 degrees C for 2.00 minutes
 PCR Cycles : 35
 Post-Extension : 72.0 degrees C for 7.00 minutes
 ForwardPrimer : GCAAGGGAT ATATATCAAG AG
 BackwardPrimer : TTCTTCAGCC GTAACCATGC



FOUNT "E63600"

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105373

General Information

JSNP ID : IMS-JST105373
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022863.5	592850	4	96928959

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022863.3	genomic	ADH7	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105373

12/17/2001

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CCAGGAAGCC AAATGTTCC ACAAGGACAC TTCAATCGTC TCAGTAGCAT GTGCTGCACT
 Observed : C/T
 3' Assay : GCTGCAGTAG TTCAATGGGA AACCAGGGTC TCATGCCCAG ATGTTGGAAG AAACGTTCCCT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_022863.3 (Graphical View of this Entry)
 Chromosome : 4
 map
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 789151 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_022863.3_20010416_20
 Amplified region : 788920..790047 in NT_022863
 size : 1128
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR "REPEAT"

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AGGCATACAG TGAGGGAAC	
BackwardPrimer	:	CAAGAGCTAC ACTGGACAC	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105382

General Information

JSNP ID : IMS-JST105382
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022863.5	572822	4	96948987

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022863.3	genomic	ADH7	intron*1	Annotated	

TCATGCTATT ATTTCAAGTA

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CTAGTTGATT TCATTGGGC TATTTTATT TCATCATAAA GCTGCTATT ATTTCAAGTA
Observed : G/A
3' Assay : GCCACAAAAT TTCCTTATT TACAGTTTTC AAGTGCTTT CTCAAATGCG CATTATTCAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_022863.3 (Graphical View of this Entry)
Chromosome : 4
map :
Definition of the record : Homo sapiens chromosome 4 working draft sequence
Position in Sequence : 809180 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_022863.3.20010416.25
Amplified region : 808358..809409 in NT_022863
size : 1052
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
 Polymerization : 72.0 degrees C for 2.00 minutes
 PCR Cycles : 35
 Post-Extension : 72.0 degrees C for 7.00 minutes
 ForwardPrimer : TGTCTAAGA GAAATGTGT GC
 BackwardPrimer : GCTTGCCAAG CTCTGTCAGA



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SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST075392

General Information

JSNP ID : IMS-JST075392
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	333322	22	40631461

Gene Information

Locus Link ID : 25830
 Gene Name : sulfortranferase family 4A, member 1
 Gene symbol : SULT4A1
 Alias symbol : SULTX3, BR-STL-1, DJ388M5.3
 Product : sulfortranferase family 4A, member 1

Relation to gene sources

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075392

12/17/2001

NT_011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology
				25830

View predicted exons with Unigene : Hs.189810

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GCCCAGACTG TCCCCCGTGT GTGCAGATTG ACTAGATCCC TGCTTCGGGC TGGGCTTGGC
 Observed : G/A
 3' Assay : GGGGCAGCTG TGCTCCAGGC ACCTCTTTT CTCTTCTGG GACTAGCAGC CTAGCCTGGG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_011521.1 (Graphical View of this Entry)
 Chromosome : 22
 map :
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 33322 (View SNP position in this record)

Method

PCR Method
 Sequence Method

NT_011521.1_20010416_5

PCR Profile

Screening region ID : NT_011521.1_20010416_5
Amplified region size : 332741..333825 in NT_011521
size : 1085

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGCTTTTCGT ACTAGAGAGT G	
BackwardPrimer	:	ACCTTCAGAC AGAGCTGGCA	



CTCTGACAG CGAAGATCAG

BackwardPrimer : CTCTGACAG CGAAGATCAG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075522

12/17/2001

NT_011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology 25830

view predicted exons with Unigene : [Hs.189810](#)

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TCTGATGCTT TCTGTGAGTT CTGGTGGGAA TTTTGATGGG CTCTGTGCCC GGTGTTGAGA
Observed : C/A
3' Assay : AGGCCATGCC CTAGAGTCCT GGRGAGTTCC ACCCCAGAAC AGCAGTGGCC TCCCCACAGGC
Comment :
Sample size : 96

Screened Sequence

Accession No. : [NT_011521.1](#) ([Graphical View of this Entry](#))
Chromosome : 22
map :
Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
Position in Sequence : 328070 ([View SNP position in this record](#))

Method

PCR Method
[Sequence Method](#)

NT_011521.1_20010416_10

PCR Profile

Screening region ID : NT_011521.1_20010416_10
Amplified region size : 327311..328210 in NT_011521
size : 900

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GCAACTGGTG AATCCTGTGA	
BackwardPrimer	:	ACACGCCACA GTCTCACAGC	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075406

General Information

JSNP ID : IMS-JST075406
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	319066	22	40617205

Gene Information

Locus Link ID : 25830
 Gene Name : sulfortranferase family 4A, member 1
 Gene symbol : SULT4A1
 Alias symbol : SULTX3, BR-STL-1, DJ388M5.3
 Product : sulfortranferase family 4A, member 1

Relation to gene sources

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075406

12/17/2001

NT_011521.1 genomic

NT_011521.1	genomic	SUL.T4A.1	intron*1	Annotated	
Hs.189810	mRNA	SUL.T4A.1	intron*3	Homology	25830

View predicted exons with Unigene : Hs.189810

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TGACCCCTCC GCTACCCCTAG ACCGCCCGTT CCCTCTGATA ACTCCACTTC CCCTGAACCC
 Observed : C/T
 3' Assay : ACCCCTTCCT TCCTCCTCTG GCCCCTTCC CTTGGCCCC ACTCCTCCCC TTGGTCTCAC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_011521.1 (Graphical View of this Entry)
 Chromosome : 22
 map :
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 319066 (View SNP position in this record)

Method

PCR Method
 Sequence Method

NT_011521.1_20010416_12

PCR Profile

Screening region ID : NT_011521.1_20010416_12
Amplified region size : 318563..319331 in NT_011521
size : 769

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCGAGACTCT CTCAGGACA	
BackwardPrimer	:	CAGGCCTTGG CATTGATGC	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075407

General Information

JSNP ID : IMS-JST075407
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	312854	22	40610993

Gene Information

Locus Link ID : 25830
 Gene Name : sulfortranferase family 4A, member 1
 Gene symbol : SULT4A1
 Alias symbol : SULTX3, BR-STL-1, DJ388M5.3
 Product : sulfortranferase family 4A, member 1

Relation to gene sources

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075407

12/17/2001

NT 011521.1 genomic

NT 011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology
				25830

view predicted exons with Unigene : Hs.189810

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CCTTCTCAGA GGCTGTACCC CCCATGGTCA GGCTTCAAG GCCTGCCGAA GCGGGGAGGG
 Observed : C/T
 3' Assay : TGGGATGGCT CAAGACGTGA GTGCCTCGGG GGCCTTTGCC AGACTTGTCC GCAGGGGATCA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT 011521.1 (Graphical View of this Entry)
 Chromosome : 22
 map :
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 312854 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011521.1_20010416_13
Amplified region : 312501..312978 in NT_011521
size : 478

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	54.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CACTTGTTAA GCGATAAAG	T
BackwardPrimer	:	ACTGTAAAGG GCTCCTGGGT	



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075407

12/17/2001

SNP Information for IMS-JST075445

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



General Information

JSNP ID : IMS-JST075445
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027064.2	268465	7	64313288

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TTTAAGGAAG GCAGCAGGAA AATAGAACAA GTGAATATTT TAYGTTCTTA GTGGTTTATG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075445

12/17/2001

PCR Conditions

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AGGTGGATGG GTGGATGACT	
BackwardPrimer	:	GAAGACGAAG TGAGAGGCTG	CT



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075475

12/17/2001

TCCTTCCCT

BackwardPrimer : ACGTATTCAG ATCCCAAATT CA



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075445

12/17/2001

SNP Information



SNP Information for IMS-JST075449

General Information

JSNP ID : IMS-JST075449
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027064.2	523034	7	64567857

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CAGCCACAAG TCCCTGGAC CTCAGAGAAT GTATATACTG TATGTGCACC CTAATAACAT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075449

12/17/2001

10035833 400701

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075449

General Information

JSNP ID : IMS-JST075449
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027064.2	523034	7	64567857

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CAGCCACAAG TCCCTGGAC CTCAGAGAAT GTATATACTG TATGTGCACC CTAATAACAT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075449

12/17/2001

FASTA SEQUENCE

Observed : A/G
 3' Assay : TTTCCTTAAA ACTAGTACTA CTGGATCCTC TAACTTTAGT ACATGTCTTT CATGTCCAAC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_007720.3 (Graphical View of this Entry)
 Chromosome : 7
 map
 Definition of the record : Homo sapiens chromosome 7 working draft sequence
 e segment.
 Position in Sequence : 411047 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_007720.3.20010416_6
 Amplified region : 410221..411418 in NT_007720
 size : 1198

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AAAGCTAAGA GTGGCCTGAG	

Variable	Mean		SD		t		p	
	Control	Case	Control	Case	Control	Case	Control	Case
Age (yr)	24.5	24.5	2.5	2.5	0.0	0.0	0.999	0.999
Sex (M/F)	10/10	10/10						
Height (cm)	170.0	170.0	5.0	5.0	0.0	0.0	0.999	0.999
Weight (kg)	65.0	65.0	10.0	10.0	0.0	0.0	0.999	0.999
Heart rate (b/min)	75.0	75.0	10.0	10.0	0.0	0.0	0.999	0.999
SBP (mmHg)	120.0	120.0	10.0	10.0	0.0	0.0	0.999	0.999
DBP (mmHg)	80.0	80.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms)	50.0	50.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b/min)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /min ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (ms ² /b ²)	100.0	100.0	10.0	10.0	0.0	0.0	0.999	0.999
HRV (b ² /ms ²)	100.0	1						

BackwardPrimer : AAGGATCTGG AAGTCTAACT G



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075449

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075465

General Information

JSNP ID : IMS-JST075465
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6176321	22	23428109

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

TCCTCTGTTGC

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GCTCTGTTGC CCAAGCTGGG TGCACCTGGTG CAGTCATAGC TACTGCAGCC TGATACTTCI
 Observed : C/T
 3' Assay : GGCTTAAGCC ATCCTCTCAC CCCAGGCTCC TGAGTAGYTA GGA CTGCAGG TGCACGCCAC
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011520.5 (Graphical View of this Entry)
 Chromosome : 22
 map :
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 6211178 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011520.5.20010417_4
 Amplified region size : 6210416..6211580 in NT_011520 : 1165
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075465

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : AAGCTCAAAG CCAACTGGTA G
BackwardPrimer : TATGTACGTT GAATCTCTGA GT



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075465

12/17/2001

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

SNP Information for IMS-JST075466

General Information

JSNP ID : IMS-JST075466
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword

search

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6176283	22	23428071

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

TCCTAGTAG

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CCTACTGCTT CTYGGCTTAA GCCATCCTCT CACCCAGGC TCCTGAGTAG
 Observed : C/T
 3' Assay : TAGGACTGCA GGTGCAGCC ACCATGCACA GCTAATTTTA ATTTTATAA AGCGGGGTC
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011520.5 (Graphical View of this Entry)
 Chromosome : 22
 map
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 6211140 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011520.5.20010417_4
 Amplified region : 6210416..6211580 in NT_011520
 size : 1165
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075466

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : AAGCTCAAAG CCAACTGGTA G
BackwardPrimer : TATGTACGTT GAATCTCTGA GT



PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GTGCAACGTG TCTCTGACTG
BackwardPrimer : AGGAGCTCA GGGAAAGTAG



SNP Information for IMS-JST105102

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105102
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	838851	11	76960358

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_009304.3	genomic	PTPNM	intron*1	Annotated	
NT_009304.3	genomic	GSTP1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105102

12/17/2001

PCR Cycle "E E E E E E E E E E"

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AAGCTCAAAG CCAACTGGTA	G
BackwardPrimer	:	TAATGACGTT GAATCTCTGA	GT



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075470

SNP Information for IMS-JST075472

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075472
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6175553	22	23427341

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075472

NT_011520.5

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TAGTTGATTT TGCAGACATC TATTATGGA AATACTCAGA GATTCAACGT ACATACCAGC
 Observed : C/T
 3' Assay : GACATTGACA GGTGAATGGC TGCACCCAG ATGTGGTTTG TTATTTTAT TATAAATATT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_011520.5 (Graphical View of this Entry)
 Chromosome : 22
 map
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 6210410 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011520.5 20010417_5
 Amplified region : 6209753..6210602 in NT_011520
 size : 850
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR-Condition

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CACCTCTCTA GCACTCACTG
BackwardPrimer : ACAGGCATGC ATGCAAACTC



SNP Information for IMS-JST075473

SNP Information



SNP Home

Search

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BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST075473
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGEASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword

search

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6175202	22	23426990

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CACCTCTCTA GCACCTCACTG
BackwardPrimer : ACAGGCATGC ATGCAAACTC



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075473

General Information

JSNP ID : IMS-JST075473
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HCBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6175202	22	23426990

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

NT_011520.5

Allele Sequence

Variation Type : SNP
 Flanking Sequence : Information
 5' Assay : CACTGTTCTC AGCCAAGGGC CCAGCAGTGG CTCTCTGGG GTCTCCTTAA AAGGTGGCTC
 Observed : G/T
 3' Assay : CTGCCCTGG CTTGCCCGAG GCTATGGGTC GGAGTTCTT GGAGTAAAGC CTGACTTTAT
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011520.5 (Graphical View of this Entry)
 Chromosome : 22
 map
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 6210059 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011520.5.20010417_5
 Amplified region : 6209753..6210602 in NT_011520
 size : 850
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Program

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CACCTCTCTA GCACCTGACTG
BackwardPrimer : ACAGGCATGC ATGCAAACTC



SNP Information for IMS-JST075475

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075475
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	6172975	22	23424763

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	TPST2	intron*1	Annotated	

TCAGCTTCCGAGGAGT

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CAGCTACTTG GGAGGCTGAG GCAGGAGAAAT CGCTTGACCC TGGGAGGCAG AGGTGCGCAGT
 Observed : G/A
 3' Assay : AGCTGAGATC ACGCCGTTGC ACTGTAGCCC GAGCGACAGA GCGAGACTCC ATCTCAAAAA
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011520.5 (Graphical View of this Entry)
 Chromosome : 22
 Map :
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 6207832 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011520.5_20010417_6
 Amplified region : 6207648..6208318 in NT_011520
 size : 671
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075475

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : AGGTGGATGG GTGGATGACT
BackwardPrimer : GAAGACGAAG TGAGAGGCTG CT



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075475

12/17/2001

SNP Information for IMS-JST105079

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

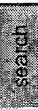
[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105079
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004966.5	3449967	1	114252371
NT_004966.5	3655834	1	114046504

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_004698.3	genomic	GSTM2	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105079

12/17/2001

NT_004698.3

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CTGGAACATC CGCGGGGTGA GCSAGGGTCC GCTGGGGCGGT GGGACGGGGG TGC GTGGGGG
 Observed : C/T
 3' Assay : GGGGAAGTGT GGAGCAGCTG CAGGACGGGC TCTAGGGACG GTTCCTCTTC AGGGCTGTCC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_004698.3 ([Graphical View of this Entry](#))
 Chromosome : 1
 map
 Definition of the record : Homo sapiens chromosome 1 working draft sequence
 Position in Sequence : 3977 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_004698.3.20010416.1
 Amplified region : 3344..4446 in NT_004698
 size : 1103

PCR Conditions

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGCTGATAAG TGACAGTGAG	
BackwardPrimer	:	CCAGCATTCT GCCTTGCAAG	



SNP Information for IMS-JST105080

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105080
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004966.5	3449104	1	114253234
NT_004966.5	3654971	1	114047367

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_004698.3	genomic	GSTM2	intron*1	Annotated	

Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	18	65	32	28	38	35	0.15	2.1	0.98	Normal
Gender	1.2	0.4	1	2	1	1	1	1	0.05	0.1	0.95	Normal
Marital Status	2.1	0.8	1	3	2	1	3	2	0.12	1.8	0.97	Normal
Education	15.8	2.5	10	20	16	15	17	16	0.08	1.5	0.99	Normal
Income	1200	300	500	2000	1100	900	1300	1000	0.18	2.5	0.96	Normal
Occupation	1.5	0.5	1	3	1	1	2	1	0.05	0.1	0.95	Normal
Health Status	2.5	0.5	1	3	2	2	2	2	0.02	0.5	0.99	Normal
Stress Level	3.2	1.0	1	5	3	2	4	3	0.15	2.1	0.98	Normal
Life Satisfaction	4.5	0.8	3	5	4	4	4	4	0.02	0.5	0.99	Normal
Work-Life Balance	3.8	0.9	2	5	3	3	4	3	0.12	1.8	0.97	Normal
Family Support	4.2	0.7	3	5	4	4	4	4	0.02	0.5	0.99	Normal
Community Involvement	2.8	0.6	1	4	2	2	3	2	0.10	1.6	0.98	Normal
Personal Growth	3.5	0.8	2	5	3	3	4	3	0.12	1.8	0.97	Normal
Overall Well-being	4.0	0.7	3	5	4	4	4	4	0.02	0.5	0.99	Normal

Allele Sequence

Variation Type	:	SNP	
Flanking Sequence	:	Information	
5' Assay	:	GGGGAAGGGG	CGTGTCTCT GACTGCATCT CCTCTCCCCA
Observed	:	G/C	
3' Assay	:	CTTAGAGGTG	TTAAGATCAG GAGTCTTCTG CCCAATTCTT CTCACTCTTG GCTGCTACAC
Comment	:		
Sample size	:	96	

Screened Sequence

```

Accession No.      : NT_004698.3 (Graphical View of this Entry)
Chromosome         : 1
map               :
Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.
Position in sequence  : 4840 (View SNP position in this record)

```

Method

PCR Method
Sequence Method

PCR Profile

```
Screening region ID : NT_004698.3_20010416_2
Amplified region   : 4010..5234 in NT_004698
size                : 1225
```

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105080

12/17/2001

PCR Program

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TAGGGACGGT TCCTCTTCAG	
BackwardPrimer	:	ATTCACTCTC AGCCTCACAG	



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105080

12/17/2001

SNP Information for IMS-JST105102

SNP Information



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General Information

JSNP ID : IMS-JST105102
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	838851	11	76960358

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_009304.3	genomic	PTPNM	intron*1	Annotated	
NT_009304.3	genomic	GSTP1	intron*1	Annotated	

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105102

NT_009304.3

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GAGATCCGAA CCCCCTTATC CCTCCGTCGT GTGGCTTTTA CCCCCGGCCT CCTTCCTGTT
 Observed : C/T
 3' Assay : CCGCCTCTC CCGCATGCC TGCTCCCCGC CCCAGTGTG TGTGAATCT TCGGAGGAAC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_009304.3 ([Graphical View of this Entry](#))
 Chromosome : 11
 map :
 Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.
 Position in Sequence : 262297 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_009304.3_20010416_3
 Amplified region : 261152..262439 in NT_009304
 size : 1288

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105102

12/17/2001

PCR Conditions

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CAGTTCGAGG TAGGACATG T	
BackwardPrimer	:	TTACTTGGCT GGTIGATGTC	



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105102

SNP Information for IMS-JST105108

SNP Information



SNP Home

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General Information

JSNP ID : IMS-JST105108
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CCCAGCCCTG AGACAGGCCG CCCGCCGCC GCAATTGGAC TAAAGAGTGT CCCAGGCGTC
Observed : C/T
3' Assay : GTGCCGCCCA ATGGGGCACA GCGGTCGGGG TCGTAGCCG CAGGGCGGTG GTCTGAGGTC
Comment :
Sample size : 96

Screened Sequence

Accession No. : AF240786.1 (Graphical View of this Entry)
 Chromosome : 22
 map : 22q11.2
 Definition of the record : Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds.
 Position in Sequence : 93402 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : AF240786.1.20000829_1
 Amplified region : 92512..93729 in AF240786
 size : 1218

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AGGACTCTGC AGTGTGAGC	
BackwardPrimer	:	AATGCAGACT GGACGAGTGC	

12/17/2001

Footnote



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105108

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SNP Information for IMS-JST105152

SNP Information



SNP Home

Search

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BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105152
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004648.5	2323162	1	165039379

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CTTCCAGCAG ATGCTTCTGT AGTATGTGAG GTTGAGAAAA AGTCGATTG TGGTCATGTA

NT_004648.3 "CE33E007"

Observed : G/T
 3' Assay : GTATAGTCAT GCCACAGTGA TGAATAATTA AAGAAAAATC TTCTAGCTCT CAGGATATGC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_004648.3 (Graphical View of this Entry)
 Chromosome : 1
 map
 Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.
 Position in Sequence : 399437 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_004648.3.20010416.8
 Amplified region : 399374..400110 in NT_004648
 size : 737

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCAAAGGTCC TAGAGCAAAG	T

TGGGTTTGGGGGGT

BackwardPrimer : AATGCATATC CTGAGAGCTA G



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105152

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SNP Information for IMS-JST104848

SNP Information



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Keyword

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General Information

JSNP ID : IMS-JST104848
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_028388.2	301178	19	71733798

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011148.3	genomic	NDUFA3	CDS*1	Annotated	

NT_011148.3

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GGGAACATGC CCGACGTGCC CAGCCACCCC CAGGAYCCTC AGGGCCCCAG CCTGGAGTGG
 Observed : C/G
 3' Assay : TGAAGAACT GTGAGCACCT CCACTGACAG AGGGGGCCCC TCCCACGGCT CCCAATAAAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_011148.3 ([Graphical View of this Entry](#))
 Chromosome : 19
 map
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
 Position in Sequence : 281924 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011148.3.20010417.3
 Amplified region : 281625..282277 in NT_011148
 size : 653
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-IST104848

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TCTTGGTCTC CATCTTCTCA G
BackwardPrimer : GTTCCTTATC TCCTGCAGAT



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SNP Information for IMS-JST104850

SNP Information



SNP Home

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Keyword



General Information

JSNP ID : IMS-JST104850
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_028388.2	300086	19	71732706

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AACTCAGCCC CAGCCCTGGC CCTCCCTT GAGTCCCCC TCCTTACCTG CACTGGCACC

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104850

TCACCTGCA CCGGGGCCAG

Observed : A/G
3' Assay : GCTCTGGAGC CCCAGTCCCT CCCCTTGAGT TCCCGCCTTC CTCACCTGCA CCGGGGCCAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_011148.3 (Graphical View of this Entry)
Chromosome : 19
map :
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
Position in Sequence : 280831 ([View SNP position in this record](#))

Method

PCR Method
[Sequence Method](#)

PCR Profile

Screening region ID : NT_011148.3.20010417.4
Amplified region : 280322..281257 in NT_011148
size : 936

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CACAGTTCTT GTCTGCCAG	

TTGAGTGGAG TGGGAGCTGA

BackwardPrimer : TTGAGTGGAG TGGGAGCTGA



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SNP Information for IMS-JST104853

SNP Information



SNP Home

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BLAST SNP

FTP Server

Search Example

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General Information

JSNP ID : IMS-JST104853
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007933.5	5088316	7	121644918

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_025775.1	genomic	NDUFA5	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104853

12/17/2001

102627 8535007

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : ATTTTCATCT TAGTTCTAAT ACTTATTGTT GGAGTGACTT GGCAATATGC TAGTTTTCTC
 Observed : G/T
 3' Assay : GTCTCAATTT CATCATCTAT AACGTGGGTA TAATAATACC CACCTCGAAC ACTTTTTGTT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_025775.1 (Graphical View of this Entry)
 Chromosome : 7
 map :
 Definition of the record : Homo sapiens chromosome 7 working draft sequence segment.
 Position in Sequence : 17431 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_025775.1.20010416.2
 Amplified region : 17117..17737 in NT_025775
 size : 621
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycle = 35

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GTCTTTATCC CAAAGGCTAG
BackwardPrimer : TCACTGTTAT AAGAGACTCA G



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104853

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SNP Information for IMS-JST104864

SNP Information



SNP Home

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General Information

JSNP ID : IMS-JST104864
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HCBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027196.2	24630	19	10190164

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CCAAAACCTC TCACCCTGGG CTTAACGAAG CCTCCCTACC ACCAACCAA GGTCTATCAA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104864

12/17/2001

TTTGGTGTCT CTTTGCACCC ACCAGCGAGC AGCCAAGCTC AGGGCAACCT CCGGGGTCTCT

Observed : A/G
 3' Assay : GGGGTGTCTCT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_027196.1 (Graphical View of this Entry)
 Chromosome : 19
 map
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
 Position in Sequence : 254198 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_027196.1_20010716_1
 Amplified region : 254003..255052 in NT_027196
 size : 1050

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCTCAAGGAG ATTGCAGCAG	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104864

12/17/2001

TCCTTCCTC CTCACCTCCG

BackwardPrimer : TTACTTCTTC CTCACCTCCG



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http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104864

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SNP Information for IMS-JST104866

SNP Information



SNP Home

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General Information

JSNP ID : IMS-JST104866
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Keyword

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Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027196.2	24966	19	10189828

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_027196.1	genomic	RPS28	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104866

12/17/2001

TCAGATTCGCGGCGG

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TAAAGGGAAC CATCAAGAAC CYGTGATGAA ATGAGAAATCG GCTCCCCGGAT TCCGGGCTGGC
 Observed : A/G
 3' Assay : GGGGTTAGGG CAGGGTAGAG GTCACATCAG GGTTAGGTC GCCGGCAGTC GCCCAAAATGC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_027196.1 (Graphical View of this Entry)
 Chromosome : 19
 map
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
 Position in Sequence : 253862 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_027196.1_20010716_2
 Amplified region : 253200..254220 in NT_027196
 size : 1021
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104866

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CCACCAACCA AAGTCTATC
BackwardPrimer : GAAATCCCAG GCCTGAGTG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST104870

General Information

JSNP ID : IMS-JST104870
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_027196.2	25572	19	10189222

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_027196.1	genomic	NDUFA7	intron*1	Annotated	

FOR "000000"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CTCCTCTCTA AGCCGGRACC CTTCGCTCTC CCGAATCTC CCTGGGAACC CCCAGCTMGT
Observed : C/G
3' Assay : ACCCTTCAG CCGGGAGCC TCTCCTGGCC TGGGAACCAAC TCAGGCCTGG GATTTCCCA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_027196.1 (Graphical View of this Entry)
Chromosome : 19
map
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
Position in Sequence : 253256 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_027196.1.20010716.3
Amplified region : 252841..253561 in NT_027196
size : 721
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "DETAILS"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CCTTTATAGG ACGTTCTAGC
BackwardPrimer : ATGTCAGCCC TCCGTTTCAG



SNP Information for IMS-JST104892

SNP Information



SNP Home

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[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST104892
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	821019	12	4611354

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TAGATGGCTC TTGTGTAGAAC AAKGCAGATT CTCAAAGGTG ACCACAGTTA AAGAAAAAT

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Income	\$10,000	\$20,000	\$5,000	\$35,000
Health status	Good	Fair	Poor	
Exercise frequency	Never	Once a week	Twice a week	Three or more times a week
Stress level	Low	Medium	High	
Sleep quality	Good	Fair	Poor	
Diet quality	Good	Fair	Poor	
Alcohol consumption	None	Occasional	Frequent	
Smoking status	Non-smoker	Smoker		
Family size	1	2	3	4
Work hours per week	40	45	30	50
Job satisfaction	High	Medium	Low	
Life satisfaction	High	Medium	Low	
Overall health score	85	10	60	100

Observed	:	T/C
3' Assay	:	ACAAGCCATT GCGCTAGAGA GAGCCATCTG CAGTTCTCC TTAGACAGAT GTTCAGATGG
Comment	:	
Sample size	:	96

Screened Sequence

Accession No.	:	NT_024413.3 (Graphical View of this Entry)
Chromosome	:	12
map	:	
Definition of the record	:	Homo sapiens chromosome 12 working draft sequence segment.
Position in sequence	:	536287 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID	:	NT_024413.3_20010417_1	
Amplified region	:	536137..536950 in NT_024413	
size	:	814	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTGAGAACAT GAGCGTGTGT	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892

12/17/2001

Forward Primer : GAGTTCCTTAA CCAGAACTGT G

Backward Primer : GAGTTCCTTAA CCAGAACTGT G



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104892

SNP Information for IMS-JST104894

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST104894
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HCBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Keyword

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	820603	12	4611770

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : ATGTGCTTGG CGGGCTCGAC GCACATTAT TTTACTTGGGA CACACCTAT TTTGGTTTCT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104894

12/17/2001

PCR "CONDITIONS"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GCTAGAAGTC CATTATCAGT C
BackwardPrimer : AGATTCCAT AATGTGGCAT G



TCGCTTACAG CTGCTTAAGA T

BackwardPrimer : TCGCTTACAG CTGCTTAAGA T



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST104894

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FOUO "SECRET"

SNP Information for IMS-JST104917

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST104917
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGEASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	806730	12	4625643

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104917

12/17/2001

NT_024413.3

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GTCCTAATAG TGGAAAGAAT GGATGCTTTA TTCACCTTGC TCFAAACTCA AAACAGGTTT
 Observed : G/A
 3' Assay : TTTGGTTATT GTTAGGCTG TTGGAGAGAA AGTAGTGAGA GATGCAITTC CGGAAGCCAT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_024413.3 ([Graphical View of this Entry](#))
 Chromosome : 12
 map
 Definition of the record : Homo sapiens chromosome 12 working draft sequence segment.
 Position in Sequence : 521998 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_024413.3.20010417.11
 Amplified region size : 521231..522366 in NT_024413 : 1136
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR "REPEAT"

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTTCCATTAT TGCAGCCTGC	
BackwardPrimer	:	GATGTAGGT GGACACAAGC A	



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



SNP Information for IMS-JST104919

General Information

JSNP ID : IMS-JST104919
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HCBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	806093	12	4626280

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	

TCATTTTTCACCTT AGCAATATGC ATTAAAGTT CTTTCATTTT TTTTCATAGC

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TAGGTGGACT TCCTTTCACCTT AGCAATATGC ATTAAAGTT CTTTCATTTT TTTTCATAGC
Observed : T/C
3' Assay : TCATAGCTCA TTTCTTTTATA TAGCTAAATA GTATTCATT GTGTATATTC CATTTGTATTG
Comment : repeat sequence (SNP is present in repeat sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_024413.3 (Graphical View of this Entry)
Chromosome : 12
map
Definition of the record : Homo sapiens chromosome 12 working draft sequence segment.
Position in Sequence : 521361 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_024413.3.20010417_11
Amplified region : 521231..522366 in NT_024413
size : 1136
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CTTCCATTAT TGCAGCTGC
BackwardPrimer : GATGTTAGGT GGACACAAGC A



SNP Information for IMS-JST104929

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST104929
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_024413.5	784948	12	4647425

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_024413.3	genomic	NDUFA9	intron*1	Annotated	

NT 024413.3

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : AGCTTCCTTT TTCAATTAAT TATACTATGC ATTAGAATGT TGTTCCTCAA GCCTTTAAAC
Observed : G/A
3' Assay : GCTGTGAAC CCTGTGCTCA CTGAAGTTTT ACCTCAAGTC CTGCTGGGTA AATCCAATAA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_024413.3 (Graphical View of this Entry)
Chromosome : 12
map
Definition of the record : Homo sapiens chromosome 12 working draft sequence segment.
Position in Sequence : 500216 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_024413.3.20010417_16
Amplified region : 499336..500446 in NT_024413
size : 1111
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "CCTT" 66336007

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CTGAGGACAC TAGAATAGAG A
BackwardPrimer : AGACAGACCG CTGTAGAGCA



SNP Information for IMS-JST105055

SNP Information



SNP Home

[Search](#)

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[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105055
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HCBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011151.5	21436	19	16971264

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011151.3	genomic	NDUFB7	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-JST105055

12/17/2001

Top of the page

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CCAGTGGCA GCGCAGCCA GAGGCGTGG GCGCGGGTG CCTGAACACC TGGCACCCCA
 Observed : G/A
 3' Assay : GGCTGGCACC CCAGGCGTGG GCTCTAACCT CAGGTGTTGT ATCTGGGTTT GGGTCTAGAC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_011151.3 (Graphical View of this Entry)
 Chromosome : 19
 map :
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
 Position in Sequence : 21436 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011151.3.20010417.1
 Amplified region : 20923..21598 in NT_011151
 size : 676
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TAGCCTCGGG CTACCAGAAG
BackwardPrimer : CTTGTGCGCT CACTTTTGCT



TOGETHER

SNP Information for IMS-JST104938

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST104938
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGEASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1022576	2	202474233

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

TTGTTGTTCC TTGTTGTTCC TTGTTGTTCC

Allele Sequence

Variation Type : SNP
 Flanking Sequence : Information
 5' Assay : TGTTTGGTCC CTGTTGTGTT AGCAATGGCT CACGCYTCG TTTGTTGTC TTTGTTGTTT
 Observed : G/T
 3' Assay : GTCCATTGAC CACGTTGGAC AGCATTTTTT TRTTCCTTTA ACTAACGGGA AATTGAGAAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_005370.2 (Graphical View of this Entry)
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 450299 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_005370.2.20010209.1
 Amplified region : 449472..450696 in NT_005370
 size : 1225
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-IST104938

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
 Polymerization : 72.0 degrees C for 2.00 minutes
 PCR Cycles : 35
 Post-Extension : 72.0 degrees C for 7.00 minutes
 ForwardPrimer : TCTTAAGTTC GTACCTCCAC G
 BackwardPrimer : GACTCAATTC TGGCTCGTAG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104938

SNP Information for IMS-JST104943

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST104943
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1032841	2	202463968

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104943

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TGATCATTCG GTATTGTTAA AACTTACAAT TTTCTTTATT TTIGAAACG AGGTCTCACT
Observed : A/G
3' Assay : TGTTGTCCAG GCTGGGCTTG AACTCCTGGC CTCAGGTGAT CATCCTGCCT CAGCCCTCCCT
Comment : repeat sequence (SNP is present in repeat sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_005370.2 (Graphical View of this Entry)
Chromosome : 2
map
Definition of the record : Homo sapiens chromosome 2 working draft sequence
Position in Sequence : 460564 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_005370.2.20010209_4
Amplified region : 459433..460769 in NT_005370
size : 1337
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : ATATCGTAGT GGAGACCTA G
BackwardPrimer : CTCCTGAGTA TCATTCTGGT A



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104943

12/17/2001

SNP Information for IMS-JST104944

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST104944
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1038241	2	202458568

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104944

12/17/2001

NT_005370.2

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GTGTTTGA GATGGAGTTT TGCTGTTGTC GCCCAGGCTG GAGTCCGCTG GCGCGATCTC
 Observed : G/A
 3' Assay : ATCTGGGTC ACTGCAGCCT CTGCCTCCTT GGTCAAGCA GTTCTCCTGC CTCATCCTCC
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_005370.2 (Graphical View of this Entry)
 Chromosome : 2
 map :
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 465964 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_005370.2.20010209.5
 Amplified region size : 465711...467023 in NT_005370 : 1313
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	\$10,000	\$20,000		
Health status	Good	Poor		
Exercise frequency	Weekly	Monthly		
Stress level	Low	High		
Sleep quality	Good	Poor		
Dietary habits	Healthy	Unhealthy		
Alcohol consumption	None	Occasional		
Tobacco use	Non-smoker	Smoker		
Family size	1-2	3-4		
Work hours	40	50		
Commuting time	30	45		
Home ownership	Owner	Renter		
Neighborhood safety	Safe	Unsafe		
Access to healthcare	Yes	No		
Health insurance	Yes	No		
Medical history	None	Chronic		
Genetic factors	None	Present		
Environmental factors	Low	High		
Social support	High	Low		
Life satisfaction	High	Low		
Overall health score	75	15	50	100

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes

ForwardPrimer : AGATACTTCA GAGGAGGTGG
BackwardPrimer : ATCAAACCCCA TTGCCTTCTC



12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST104947

General Information

JSNP ID : IMS-JST104947
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HCBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1039346	2	202457463

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NIDUFS1	intron*1	Annotated	

NT_005370.2

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GGCAATGGGT TTGATGATAG GAGAATATTT CATGGATCT CTGTATGCT TAAATTTAAA
 Observed : G/T
 3' Assay : TAAATTTGCA TTTTATATAT TGTATTCTCA GCACAGATTT GCGTTCCAAAT TATCTTCTTA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_005370.2 (Graphical View of this Entry)
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 467069 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_005370.2.20010209_6
 Amplified region : 466599..468073 in NT_005370
 size : 1475
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

[illegible]

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes

ForwardPrimer : AGACCAAGAT CAAACCAGAA G
BackwardPrimer : AAGGAGAGGA GAAAACGGAC



12/17/2001

SNP Information for IMS-JST104949

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST104949
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1048121	2	202448688

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005370.2	genomic	NDUFS1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104949

12/17/2001

NT_005370.2

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CTGACCACAG GATAATTTGC TAGGCTTTT ATTCTGAATA ATTACTTTTA GAAAACGTGT
 Observed : T/C
 3' Assay : TTAGCTGATA CTCAGGCATA TTTCACAGTA GCATTGGCAA GATGCTTTGG ATTAAACTAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_005370.2 (Graphical View of this Entry)
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 475844 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_005370.2.20010209_7
 Amplified region : 475669..476952 in NT_005370
 size : 1284
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104949

PCR Cycling Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : GTAGATGGAA GATAGTAGGC A
BackwardPrimer : AGGATCAGTT CCATTCTGC AC



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104949

12/17/2001

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

SNP Information for IMS-JST104958

General Information

JSNP ID : IMS-JST104958
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005370.5	1057719	2	202439090

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GGGTAAATAG GAAAAATACA TAATCATGCT CAGATATGTA TCTAGGATAA TTATAATTAA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104958

12/17/2001

TTAGCTTTA TTAGCTTTA TTATGTGC TAAGCACTCT

Observed : T/A
3' Assay : AATAATCATA GTAACAATGG CTAATGATAA TTAGCTTTA TTATGTGC TAAGCACTCT
Comment : repeat sequence (repeat sequence exists in flanking sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_005370.2 (Graphical View of this Entry)
Chromosome : 2
map
Definition of the record : Homo sapiens chromosome 2 working draft sequence
e segment.
Position in Sequence : 485442 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_005370.2 20010209_11
Amplified region : 484655..485807 in NT_005370
size : 1153

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extention	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GCATACTGGT GCACGTGCTA	

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104958

TGAGT" CCGGGGT

BackwardPrimer : ACCATGACAT TATAGAGCA GA



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104958

12/17/2001

SNP Information for IMS-JST104960

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST104960
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008978.5	308976	11	46472116

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_008956.3	genomic	MTCH2	intron*1	Annotated	
NT_008956.3	genomic	NDUFS3	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104960

12/17/2001

For "CE36001"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CGGCGCTGAC CAGGGGTGAG CACGGGCAGC CAGCTGAGAC CGGGGTGAGG CGCAGCGGCG
Observed : T/C
3' Assay : GCCCAGTGCA GAGAGCTCCT CAGGGCTCAT CCGCGGCGTC TGTGCTTTT ATCTCCCTGT
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_008956.3 ([Graphical View of this Entry](#))
Chromosome : 11
map
Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.
Position in Sequence : 737571 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_008956.3.20010416.2
Amplified region : 736668..737858 in NT_008956
size : 1191

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104960

12/17/2001

Forward Primer

Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGTCTCGCTT TCTCACTGC
BackwardPrimer : CTTGAAGATC CCTCACAGAC



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104960

SNP Information for IMS-JST104978

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST104978
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006693.5	251179	5	48905237

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006693.3	genomic	NDUFS4	intron*1	Annotated	

TOP SECRET

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTTAATAGAC AAATTCTCTCA ACTGATAATT CAAAGTTCTT CACAATATAG GCACAAACTT
Observed : A/C
3' Assay : CTACCAAAGC ACTAACAAGT TTTGTCTCTG TTCCAACCTCT TACTTCTGC CCTTACATTG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006693.3 (Graphical View of this Entry)
Chromosome : 5
map
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.
Position in Sequence : 754982 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006693.3_20010416_9
Amplified region : 754001..755125 in NT_006693
size : 1125
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
 Polymerization : 72.0 degrees C for 2.00 minutes
 PCR Cycles : 35
 Post-Extension : 72.0 degrees C for 7.00 minutes
 ForwardPrimer : ACTGTTACGT ATACTGCCTC A
 BackwardPrimer : ACTAGCATCA TAGTACCAGG A



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST104978

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SNP Information for IMS-JST104980

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST104980
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006693.5	253052	5	48907110

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006693.3	genomic	NDUFS4	intron*1	Annotated	

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104980

TOP SECRET

Allele Sequence

Variation Type : SNP
 Flanking Sequence : Information
 5' Assay : TACACAAAGTT CCCCCATTAA TCATCTGTTT TCAGTIGTTA ACCAAATAAG GTATTATGCA
 Observed : G/A
 3' Assay : GCTCATCTTT TTATATAAGA ATACTCTACT CTTGTTTTTG AGATGAAAAG AAGTTCTCTT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006693.3 (Graphical View of this Entry)
 Chromosome : 5
 Map :
 Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.
 Position in Sequence : 753109 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006693.3_20010416_10
 Amplified region : 752239..753543 in NT_006693
 size : 1305
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

PCR "EE3E00"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCTTCAGGTA CTCTTACCTA G
BackwardPrimer : CGTGCCTTCTA CCTTCTATTA C



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104980

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST104982

General Information

JSNP ID : IMS-JST104982
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006693.5	259294	5	48913352

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006693.3	genomic	NDUFS4	intron*1	Annotated	

TOGETHER

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : ACCTTATTG CTTGTTTAA TCACTTTATA TAAATTTTCAAT GGAAGACTT GCTTTGCCAG
 Observed : T/C
 3' Assay : GTATCCGAAA CCTCTGTTAT TTCTCCATAG TATTTTCTAT AGAAGATCTA GGATACTTTT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006693.3 (Graphical View of this Entry)
 Chromosome : 5
 map
 Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.
 Position in Sequence : 746867 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006693.3.20010416.11
 Amplified region : 746420..747407 in NT_006693
 size : 988
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST104982

PCR CONDITIONS

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TCCTGGATCC TGTCTGTAGC	
BackwardPrimer	:	CTGACATGAG TTGGGAAGTG A	



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST104982

12/17/2001

SNP Information for IMS-JST105004

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105004
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004893.5	9766	1	39174537

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : AGTAGTTCTA CTATAAAGGA ACTCATTTAA CTTTGCTTAA CCCAACAGCT CCCAATGTAA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105004

12/17/2001

TTGAGCTTGGGCT

Observed : A/G
 3' Assay : ACAGATCTAT TAAATTTCTG AGGAACCCAG TTGTATGGGT CACCAGACTA GGAACAATA
 Comment : repeat sequence (repeat sequence exists in flanking sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_004893.3 (Graphical View of this Entry)
 Chromosome : 1
 map
 Definition of the record : Homo sapiens chromosome 1 working draft sequence
 e segment.
 Position in Sequence : 969241 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_004893.3 20010416_6
 Amplified region : 968721..969831 in NT_004893
 size : 1111

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGGGATGGC TAGAAAGCTA	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105004

12/17/2001

TGCTAAAC TCTCAACAGG T

BackwardPrimer : TGCTAAAC TCTCAACAGG T



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105004

12/17/2001

SNP Information for IMS-JST105012

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

Search

General Information

JSNP ID : IMS-JST105012
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004893.5	42727	1	39141576

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TGCAATTGGCA CGATCTTGGC TCACTGCAAC CACCATCTCC CAGATTCAAG TGGTTCTCCT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105012

12/17/2001

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male	Female	Male	Female
Marital status	Married	Single	Married	Single
Education	High school	College	High school	College
Occupation	Manager	Worker	Manager	Worker
Income	\$10,000	\$20,000	\$10,000	\$20,000
Health status	Good	Fair	Good	Fair
Exercise frequency	Weekly	Monthly	Weekly	Monthly
Stress level	Low	High	Low	High
Smoking status	Smoker	Non-smoker	Smoker	Non-smoker
Alcohol consumption	Regular	Occasional	Regular	Occasional
Family size	2	3	2	3
Home ownership	Owner	Renter	Owner	Renter
Commute time	30 min	45 min	30 min	45 min
Work hours	40 hrs	50 hrs	40 hrs	50 hrs
Job satisfaction	High	Low	High	Low
Life satisfaction	High	Low	High	Low
Overall health	Good	Fair	Good	Fair

```

Accession No.      : NT_004893.3 (Graphical View of this Entry)
Chromosome        : 1
map              :
Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.
Position in Sequence : 958402 (View SNP position in this record)

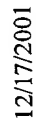
```

PCR Method
Sequence Method

Screening region ID	:	NT_004893.3	20010416_10
Amplified region	:	958036..958985	in NT_004893
size	:	950	
Pre-Denature	:	94.0 degrees C	for 2.00 minutes
Denaturation	:	94.0 degrees C	for 0.50 minutes
Annealing	:	60.0 degrees C	for 0.50 minutes
Polymerization	:	72.0 degrees C	for 2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C	for 7.00 minutes
ForwardPrimer	:	TCAGAGAGGT	TATGTATACT"

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105012

BackwardPrimer : AACACTATCA TTTCTTAAT GAG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105012

SNP Information for IMS-JST105024

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

JSNP ID	:	TMS-JST105024
dbSNP ID(rs#)	:	
dbSNP ID(ss#)	:	
HGBASE ID	:	
Organism	:	Homo sapiens
Molecular type	:	Genomic
Laboratory	:	Laboratory for
Citation	:	J Hum Genet.
Release Date	:	2001/08/09
Last Update	:	2001/08/09

NEW Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029292.1	199159	5	63454372

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006455.3	genomic	NDUFS6	intron *1	Annotated	

NT_006455.3

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GCACTGAGCT CCTGGAGCCA GACGTTTGCT GGTGATGGC GGTGAGGTC ACCCTTGAGC
Observed : T/C
3' Assay : GCGCACACTA AATGACGGGA GGGCATCCGG CGTCAGTCRC CAGTGTCGAG GCGTCAGCAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006455.3 (Graphical View of this Entry)
Chromosome : 5
map
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.
Position in Sequence : 219541 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006455.3_20010416_4
Amplified region : 219323..220443 in NT_006455
size : 1121
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

--- SNP INFORMATION ---

PCR REACTION

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : ATCCACAT TCTCAAAGCA AG
BackwardPrimer : CTGCTGCAGG CGATGCAACT



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105024

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



SNP Information for IMS-JST105029

General Information

JSNP ID : IMS-JST105029
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029292.1	194050	5	63449263

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006455.3	genomic	NDUFS6	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105029

12/17/2001

NT_006455.3

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TACAGCGCCA CACTACAGGG CCTACATAGA GCGGCCTGTC CGAARACCCC CTTTCAACTG
Observed : T/C
3' Assay : GAAAGTGGTGG GCGGCATGTT TCTCTTCTCG GAGGCCCAAG CGTCITTCCT CTCTGGGCCC
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006455.3 (Graphical View of this Entry)
Chromosome : 5
map :
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.
Position in Sequence : 214432 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006455.3_20010416_7
Amplified region : 213959..214961 in NT_006455
size : 1003
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GCGTTTGGAA CTTTATTCCA GT
BackwardPrimer : GTCCTGTATA TGACACTCAT C



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105029

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105030

General Information

JSNP ID : IMS-JST105030
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029292.1	193227	5	63448440

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006455.3	genomic	NDUFS6	intron *1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105030

12/17/2001

TOP SECRET

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GAAAAGGGGA CAGTCTAACA GGCATAAATG GTTAAGCAGC CTAGAGTGGG ACTGGGCACC
Observed : C/T
3' Assay : GGCATGTCCC CTCTGGGCT CCAGCCCTGA AGCCCAAGCC TGGTTGTGCC TCACTGTTCGT
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006455.3 ([Graphical View of this Entry](#))
Chromosome : 5
map
Definition of the record : Homo sapiens chromosome 5 working draft sequence segment.
Position in Sequence : 213609 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006455.3.20010416.8
Amplified region : 212603..213807 in NT_006455
size : 1205
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105030

12/17/2001

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CACCGACAGT GGAGCACTCA G
BackwardPrimer : ATGTGACTTT CGATGCTTC A



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105030

SNP Information for IMS-JST105031

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105031
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029292.1	192402	5	63447615

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GGAGAAGGAG AAGTGCCTCT TGTTTTGCAG ATGCAACTGT GCTTCAGAGA GCCAAGGTGG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105031

12/17/2001

FOOTER "663600"

Observed : A/G
3' Assay : ATGTGACCTC TCCACATTC TCCGGTGCTG TGATGTACCT TAAACACAGC AAGGTACTTG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Homo sapiens chromosome 6 working draft sequence
segment.
Position in Sequence : 183417 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_026300.1_20010416_4
Amplified region : 182827..184053 in NT_026300
size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

Sequence

BackwardPrimer : ATGTGACTTT CGATGCTTC A



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105031

SNP Information



SNP Home

Search

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FTP Server

Search Example

General Information

JSNP ID : IMS-JST105033
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	1341784	11	76457425

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CCCCCTGGCT CACTCAGGAT CCGCGGCCCTC CGTGTCTTTC AGGTGCAGCG GGGAGCCGGC

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105033

12/17/2001

TOGETHER

Observed : T/C
 3' Assay : CTCAGGGCGC ATGCGCGGCC CGTCTGTGGC CACCGGCCTA GTTAGGTCG GAGATCACTG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_008940.3 (Graphical View of this Entry)
 Chromosome : 11
 map
 Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.
 Position in Sequence : 752973 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_008940.3_20010416_1
 Amplified region : 752610..753519 in NT_008940
 size : 910

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymorization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	ATCTCGTCGC	CATTACCGTC

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105033

12/17/2001

TCCTCGGTA "CCACATTCCT"

BackwardPrimer : GTCTCGGTA CCACATTCCT



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105033

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105036

General Information

JSNP ID : IMS-JST105036
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	1343347	11	76455862

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_008940.3	genomic	NDUFS8	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105036

12/17/2001

NT_008940.3

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GAGACCTGAG TTCCAGTCCT GGCATTGTCA GGGCGTTCT TCTCTGAGCC TGTTCCTCACT
Observed : T/C
3' Assay : TTAAATGAT TATGTGATG GAGACTGACT CTGATTCACA GGGCAGGGT CCATCATTGC
Comment : repeat sequence (repeat sequence exists in flanking sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_008940.3 (Graphical View of this Entry)
Chromosome : 11
map
Definition of the record : Homo sapiens chromosome 11 working draft sequence segment.
Position in Sequence : 751410 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_008940.3_20010416_2
Amplified region : 751038..752167 in NT_008940
size : 1130
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR program

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GGAGTCCTTG TAAGGATAGG A
BackwardPrimer : GGTCGCAACTG CTGGGCTACA



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105036

TOGETHER

SNP Information for IMS-JST105043

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

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General Information

JSNP ID : IMS-JST105043
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008940.5	1349122	11	76450087

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CCAGGCCCGG CTCTGGGGCT CCACTTGTC ACCCTGCCG CAGCCCCACA GGCCTGTGCT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105043

12/17/2001

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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Observed	:	C/A
3' Assay	:	GCTGTGTGGG GCTTAGGGAT CACCAGRGCT GAAGGGCCCC TGGGCTCCAG TGGGAATGCC
Comment	:	
Sample size	:	96

Screened Sequence

```

Accession No.      : NT_008940.3 (Graphical View of this Entry)
Chromosome         : 11
map               :
Definition of the record : Homo sapiens chromosome 11 working draft sequen
                    : ce segment.
Position in Sequence : 745636 (View SNP position in this record)

```

Method

PCR Method	Sequence Method
------------	-----------------

PCR Profile

Screening region ID	:	NT 008940.3-20010416.5	
Amplified region	:	745238..746342 in NT_008940	
size	:	1105	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCAGTCAGTG TTGGAATGC	T

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105043

12/17/2001

Forward Primer : GGTGCTTACA CCTTCCTGCT

Backward Primer : GGTGCTTACA CCTTCCTGCT



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105043

SNP Information



SNP Home

[Search](#)

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[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075272
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40.
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	681007	6	2980483

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GCAACTCCTA GAGGGGTCCT TGGGGAGACG CGGGTCCCAG TCCTGGGGCT CCTACTGGGG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075272

12/17/2001

Observed	:	A/C
3' Assay	:	GTGGCGTGGT CGGAAGGTGA GTGATCCCT GTCGGGACC GGGGACTTG GGAAGGACAG
Comment	:	
Sample size	:	96

```

Accession No.      : NT_026300.1 (Graphical View of this Entry)
Chromosome        : 6
map              :
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 187084 (View SNP position in this record)

```

PCR Method
Sequence Method

Screening region ID	:	NT_026300.1.20010416_2	
Amplified region	:	186698..187589 in NT_026300	
size	:	892	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TATCAATCCA GTTTCACCT	G

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075272

12/17/2001

Sequence: CCGGCGTT

BackwardPrimer : CAGCGCAAC CAGTGGTTCA



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075272

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075273
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	682942	6	2978548

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTCCCCACT ATTCAAATA GTATAGAAA TAGAGTGAG TCACTCAAT AGAGTGAGT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075273

12/17/2001

TOGETHER

Observed : T/C
3' Assay : AGTCACTCAG CTCTTGGACC TCAGATTCTT ATTCTTAACC GCTAGGGGA TGGAGACAGA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
Chromosome : 6
map :
Definition of the record : Homo sapiens chromosome 6 working draft sequence
e segment.
Position in Sequence : 185149 ([View SNP position in this record](#))

Method

PCR Method
[Sequence Method](#)

PCR Profile

Screening region ID : NT_026300.1.20010416_3
Amplified region : 184926..185711 in NT_026300
size : 786

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	ATCTCCGAAG ATCAGACCA	

BackwardPrimer : AGTGATTGCC CGAAATCATG



SNP Information for IMS-JST075274

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075274
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	683027	6	2978463

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ATTCTTATTC TTAACCGCTA GGGGGATGGA GACAGAAGTC ACAAACTCAC ATGCCACCAG

10036839 100701

12/17/2001 12:33:00

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075584

General Information

JSNP ID : IMS-JST075584
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	419468	4	68119470

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

Observed	:	C/G
3' Assay	:	CATATGATGT AATCATGTAA ACTGGGCCAA GGAATACAAA AGGAGTGGT GAGCTGGGGA
Comment	:	
Sample size	:	96

```

Accession No.      : NT_026300.1 (Graphical View of this Entry)
Chromosome         : 6
map               :
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 185064 (View SNP position in this record)

```

<u>PCR Method</u>	
Sequence Method	

Screening region ID	:	NT_026300.1.20010416_3
Amplified region	:	184926..185711 in NT_026300
size	:	786
Pre-Denature	:	94.0 degrees C for 2.00 minutes
Denaturation	:	94.0 degrees C for 0.50 minutes
Annealing	:	60.0 degrees C for 0.50 minutes
Polymerization	:	72.0 degrees C for 2.00 minutes
PCR Cycles	:	35
Post-Extension	:	72.0 degrees C for 7.00 minutes
ForwardPrimer	:	ATCTCCGAAG ATCACAGCCA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075274

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	1.5	0.5	1	2
Health status	1.5	0.5	1	2
Life satisfaction	1.5	0.5	1	2
Life expectancy	1.5	0.5	1	2
Life expectancy squared	1.5	0.5	1	2
Life expectancy cubed	1.5	0.5	1	2
Life expectancy to the power of 4	1.5	0.5	1	2
Life expectancy to the power of 5	1.5	0.5	1	2
Life expectancy to the power of 6	1.5	0.5	1	2
Life expectancy to the power of 7	1.5	0.5	1	2
Life expectancy to the power of 8	1.5	0.5	1	2
Life expectancy to the power of 9	1.5	0.5	1	2
Life expectancy to the power of 10	1.5	0.5	1	2
Life expectancy to the power of 11	1.5	0.5	1	2
Life expectancy to the power of 12	1.5	0.5	1	2
Life expectancy to the power of 13	1.5	0.5	1	2
Life expectancy to the power of 14	1.5	0.5	1	2
Life expectancy to the power of 15	1.5	0.5	1	2
Life expectancy to the power of 16	1.5	0.5	1	2
Life expectancy to the power of 17	1.5	0.5	1	2
Life expectancy to the power of 18	1.5	0.5	1	2
Life expectancy to the power of 19	1.5	0.5	1	2
Life expectancy to the power of 20	1.5	0.5	1	2
Life expectancy to the power of 21	1.5	0.5	1	2
Life expectancy to the power of 22	1.5	0.5	1	2
Life expectancy to the power of 23	1.5	0.5	1	2
Life expectancy to the power of 24	1.5	0.5	1	2
Life expectancy to the power of 25	1.5	0.5	1	2
Life expectancy to the power of 26	1.5	0.5	1	2
Life expectancy to the power of 27	1.5	0.5	1	2
Life expectancy to the power of 28	1.5	0.5	1	2
Life expectancy to the power of 29	1.5	0.5	1	2
Life expectancy to the power of 30	1.5	0.5	1	2
Life expectancy to the power of 31	1.5	0.5	1	2
Life expectancy to the power of 32	1.5	0.5	1	2
Life expectancy to the power of 33	1.5	0.5	1	2
Life expectancy to the power of 34	1.5	0.5	1	2
Life expectancy to the power of 35	1.5	0.5	1	2
Life expectancy to the power of 36	1.5	0.5	1	2
Life expectancy to the power of 37	1.5	0.5	1	2
Life expectancy to the power of 38	1.5	0.5	1	2
Life expectancy to the power of 39	1.5	0.5	1	2
Life expectancy to the power of 40	1.5	0.5	1	2
Life expectancy to the power of 41	1.5	0.5	1	2
Life expectancy to the power of 42	1.5	0.5	1	2
Life expectancy to the power of 43	1.5	0.5	1	2
Life expectancy to the power of 44	1.5	0.5	1	2
Life expectancy to the power of 45	1.5	0.5	1	2
Life expectancy to the power of 46	1.5	0.5	1	2
Life expectancy to the power of 47	1.5	0.5	1	2
Life expectancy to the power of 48	1.5	0.5	1	2
Life expectancy to the power of 49	1.5	0.5	1	2
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Life expectancy to the power of 51	1.5	0.5	1	2
Life expectancy to the power of 52	1.5	0.5	1	2
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Life expectancy to the power of 54	1.5	0.5	1	2
Life expectancy to the power of 55	1.5	0.5	1	2
Life expectancy to the power of 56	1.5	0.5	1	2
Life expectancy to the power of 57	1.5	0.5	1	2
Life expectancy to the power of 58	1.5	0.5	1	2
Life expectancy to the power of 59	1.5	0.5	1	2
Life expectancy to the power of 60	1.5	0.5	1	2
Life expectancy to the power of 61	1.5	0.5	1	2
Life expectancy to the power of 62	1.5	0.5	1	2
Life expectancy to the power of 63	1.5	0.5	1	2
Life expectancy to the power of 64	1.5	0.5	1	2
Life expectancy to the power of 65	1.5	0.5	1	2
Life expectancy to the power of 66	1.5	0.5	1	2
Life expectancy to the power of 67	1.5	0.5	1	2
Life expectancy to the power of 68	1.5	0.5	1	2
Life expectancy to the power of 69	1.5	0.5	1	2

BackwardPrimer : AGTGATTGCC CGAAATCATG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075274

12/17/2001

SNP Information for IMS-JST075276

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075276
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	684479	6	2977011

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CTGCCCTAG GCTAGGAGAG CTGGCAATG CCTGGAGACC CAAAGGCCTC ATCCTCAGGG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075276

12/17/2001

Sequence

Observed : C/A
3' Assay : GGCCAACTCT TCTGTTTAG TGATATACAG ACTATCTTTT ATTGTGATTT ATAGTCCAAC
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Homo sapiens chromosome 6 working draft sequence
e segment.
Position in Sequence : 183612 ([View SNP position in this record](#))

Method

PCR Method
[Sequence Method](#)

PCR Profile

Screening region ID : NT_026300.1 20010416_4
Amplified region : 182827..184053 in NT_026300
size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

12/17/2001

[illegible]

BackwardPrimer : ACTGGACAGC TGGGAACCTG



12/17/2001

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SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075279

General Information

JSNP ID : IMS-JST075279
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	684621	6	2976869

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CCTGTATTCA TAAACTTTCT TTTTCCTTTC CTTCCTCACT GCCCAGCTTT AGGTTCAYYC

TTTGAAGGGA TGAATGTGAC

Observed : T/C
 3' Assay : TGTAAGTGTG GCTGGTGTCA GAATAGGAAC CTCCTGCGC TTTGAAGGGA TGAATGTGAC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
 Chromosome : 6
 map
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
 Position in Sequence : 183470 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_026300.1_20010416_4
 Amplified region : 182827..184053 in NT_026300
 size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075279

12/17/2001

Forward Primer : TGGGACCTG

BackwardPrimer : ACTGGACACG TGGGACCTG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075279

Top of Page

SNP Information for IMS-JST075280

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST075280
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	684674	6	2976816

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TTCAATCTTG TAAGTGTTGC TGGTGTGAGA ATAGGACCT CCCTGGGCTT TGAAGGGATG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075280

12/17/2001

TOGETHER WE CAN SAVE LIVES

Observed : A/G
3' Assay : ATGTGACCTC TCCACATTC TCCGGTGCTG TGATGTACCT TAAACACAGC AAGGTACTTG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Homo sapiens chromosome 6 working draft sequence
Position in Sequence : 183417 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_026300.1_20010416_4
Amplified region : 182827..184053 in NT_026300
size : 1227

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTCCAGGCAG TGACTGTCCA	

TCCTTCCCT

BackwardPrimer : ACTGGACAGC TGGGAACCTG



12/17/2001

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SECRET

SNP Information for IMS-JST075282

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075282
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword

Search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	687511	6	2973979

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075282

12/17/2001

NT_026300.1

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : ACCCATCAA TCAGAGAGAA GGAATCCACC TTCTTAGCT ATGGCAGGTA ATGATTCACCT
 Observed : A/G
 3' Assay : TTGTGGAGTA AGACTTTTT TTTTGTGAGA TGGGATTTTG TTGTATTGCC CAGGCTGGTC
 Comment : repeat sequence (repeat sequence exists in flanking sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
 Chromosome : 6
 map
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
 Position in Sequence : 180580 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_026300.1_20010416_6
 Amplified region : 179255..180775 in NT_026300
 size : 1521
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075282

12/17/2001

PCR Condition

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGTCAGGAAG CAGCAGTGAT
BackwardPrimer : ACATTGCAG ATATCAGCTA C



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075284

General Information

JSNP ID : IMS-JST075284
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	688132	6	2973358

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075284

12/17/2001

NT_026300.1

Allele Sequence

Variation Type : SNP
 Flanking Sequence : Information
 5' Assay : CTGGGCCAGA TAATCCTATG TTTTGGGGG TCATCCTGTG CACCTGTTT AGCACCTAGC
 Observed : A/C
 3' Assay : CCATCCCTGG CCTCTGCCCA CCAGATGCCA GTAGCACCCC TCCCCCACCG GCTGTGACAA
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
 Chromosome : 6
 map
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
 Position in Sequence : 179959 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_026300.1_20010416_6
 Amplified region : 179255..180775 in NT_026300
 size : 1521
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGTCAGGAAG CAGCAGTCAT
BackwardPrimer : ACATTGCAG ATATCAGCTA C



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075284

12/17/2001

SNP Information for IMS-JST075286

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST075286
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword

Mapping Information NEW

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
U07736.1	genomic	NQ02	CDS*1	Annotated	
U07732.1	genomic	NQ02	exon*1	Annotated	

Allele Sequence

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075286

12/17/2001

Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GTAGATGAAC TGAGCAGGCA GGGCTGCACC GTCACAGTGT CTGATTGTA TGCCATGAAC
Observed : T/C
3' Assay : TTGAGCCGAG GGCCACAGAC AAAGATATCA CTGGTGAGTC ATGGGATAAA TGCTCTATTT
Comment :
Sample size : 96

Screened Sequence

Accession No. : U07732.1 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Human quinone oxidoreductase2 (NQO2) gene, introns 2 and 3 and exon 3.
Position in Sequence : 372 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : U07732.1.20000425_1
Amplified region : 21..552 in U07732_1
size : 532
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35

FORGET THE ROOT

Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TTGCAGTCAG CTGAGTCATG C
BackwardPrimer : GTGATAATCC CAGTGCTATC TA



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075286

12/17/2001

SNP Information for IMS-JST075290

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST075290
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	695442	6	2966048

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

FOREFORE

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ACGCTGAGCT CTCTGTCTGT CTTCTCTCTGT CCCCTTTGGG TCGGCCGGCC ACGTGGAGCC
Observed : C/T
3' Assay : GCTTTCCTCC TCGCAGCCAC TCCACTCCCA TAACCCGGTG GCTGGGTAGG CTAAGACCTG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 172649 (View SNP position in this record)

Method

PCR Method
Sequence Method

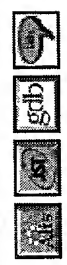
PCR Profile

Screening region ID : NT_026300.1_20010416_8
Amplified region : 172424..173856 in NT_026300
size : 1433
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "SCREENING"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TATCCACGTA GCCAATATCA C
BackwardPrimer : GCTCTGATAT TAGTAGTGCA G



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075290

12/17/2001

Top of Page

SNP Information for IMS-JST075291

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST075291
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	696193	6	2965297

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

NT_026300.1

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TCCTTTTGAC TGGCTTGATC ACAGACTGCT GCTCAAAGC TGGTGTACG CACAGCTCCT
Observed : C/T
3' Assay : GTCCCTCCC TGCCTGCCA GGGCCAGCAT CAGGGGCTGT CATCACTGGG GGATGCAGAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 171898 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_026300.1_20010416_9
Amplified region : 171031..172143 in NT_026300
size : 1113
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "E3E00T"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CGGTAACACT GGATGTAATG T
BackwardPrimer : TCATAGCTAC CACATGTGGC A



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12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075292

General Information

JSNP ID : IMS-JST075292
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	696494	6	2964996

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	CDS*1	Annotated	

NT_026300.1

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AGCCTCAGTT TCTCTTTGGT GTTCCCGCCC ACAGTTCCCG CTGTACTGGT TCAGCGTGCC
 Observed : A/G
 3' Assay : GCCATCCTGA AGGGCTGGAT GGATAGGGTG CTGTGCCAGG GCTTTGCCTT TGACATCCCA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 (Graphical View of this Entry)
 Chromosome : 6
 map
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
 Position in Sequence : 171597 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_026300.1.20010416.9
 Amplified region : 171031..172143 in NT_026300
 size : 1113
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075292

12/17/2001

PCR Settings

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CGGTAACACT GGATGTAATG T
BackwardPrimer : TCATAGCTAC CACATGTGGC A



SNP Information for IMS-JST075294

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075294
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_026300.3	696602	6	2964888

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_026300.1	genomic	NMOR2	intron*1	Annotated	

104347 "CCGCGGT"

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CTTTGACATC CCAGGATTCT ACGATTCCGG TTTCCTCCAG GTATGTGCTC TTGGATAAGG
 Observed : A/T
 3' Assay : TCACATATGGA TAGTTGGAGG GAGGGACACAG AGGATGCGTC TTCTATCAAG TTATAATTTCT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_026300.1 ([Graphical View of this Entry](#))
 Chromosome : 6
 map
 Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
 Position in Sequence : 171489 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_026300.1 20010416_9
 Amplified region : 171031..172143 in NT_026300
 size : 1113
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

Table 1

Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CGGTAACACT GGATGTAATG	T
BackwardPrimer	:	TCATAGCTAC CACATGTGGC	A



TCCTGCTGT

BackwardPrimer : AGGTGGAGAT TCCTGCTGT



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12/17/2001

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

search

General Information

JSNP ID : IMS-JST075348
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_029462.1	51841	16	72320063

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_010441.3	genomic	LOC82562	CDS*1	Annotated	

NT_010441.3 "CE33600T"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TGGGGACTGG AAGACCACCT TCACCGTGGC GCAGAATGAG CGCTTCGATG CGGACTATGC
Observed : G/A
3' Assay : GACAAGATGG CAGGCTGCAG CCTCAGCTTC CGCTCTGAGC TGTGAGAGGG GCTCCTGGAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_010441.3 (Graphical View of this Entry)
Chromosome : 16
map :
Definition of the record : Homo sapiens chromosome 16 working draft sequence segment.
Position in Sequence : 25476 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_010441.3.20010416.1
Amplified region : 24795..25705 in NT_010441
size : 911
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "E3E0T"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GAGTCATGG ACCACAGCAI
BackwardPrimer : ACTCGACGTC CTCACCATC



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075348

12/17/2001

TEXT "663300"

SNP Information for IMS-JST075350

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075350
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40.
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	351246	4	68051248

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

TCCTTTTGCATGAGAAACATTAAAA TAGTCATTTA

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTAGACTTAC TAGTTATTGA TACCTCTTTG GCATGAGAA AACATTAAAA TAGTCATTTA
Observed : T/C
3' Assay : AGCAATGCAC AGGTATAATA AAACCTCCAA TTATTAAAGA GGGTATTATT ATCTCTCCTT
Comment : repeat sequence (repeat sequence exists in flanking sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
Chromosome : 4
map
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
Position in Sequence : 1248731 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416_2
Amplified region : 1248329..1249405 in NT_006281
size : 1077
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
 Polymerization : 72.0 degrees C for 2.00 minutes
 PCR Cycles : 35
 Post-Extension : 72.0 degrees C for 7.00 minutes
 ForwardPrimer : GCCTTCTAT TCAGAGATGG C
 BackwardPrimer : CTGAGGTTG GATTCTGTG C



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075350

12/17/2001

SNP Information



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[FTP Server](#)

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SNP Information for IMS-JST075352

General Information

JSNP ID : IMS-JST075352
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	339744	4	68039746

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

NT_006281.3

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTTTGGAGGT CAGTGTATTT TTGCTGAAA TGCTTTCCTT GTACTTGACA TTAATAAATA
Observed : T/C
3' Assay : CTGATGTTT TATATCCATA AATAGCTAAT TTTACTTTT AGATTGTCC TCATATTSTT
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
Chromosome : 4
map :
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
Position in Sequence : 1260233 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3 20010416_3
Amplified region : 1260005..1261237 in NT_006281
size : 1233
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "CONDITIONS"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GCTAGAAGTC CATTATCAGT C
BackwardPrimer : AGATTCCAT AATGTGGCAT G



SNP Information



SNP Home

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SNP Information for IMS-JST075355

General Information

JSNP ID : IMS-JST075355
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	339588	4	68039590

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075355

12/17/2001

Sequence

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : AATTGATTT ACTATTTCAGA CAGAAATATT TAATTGATG AATGTTTATG AAAATAGACT
Observed : T/C
3' Assay : TTATCTGGTT TTAGTGGCCT ATGGTTCCTG GTTTACTCAT GTTAAAAAACT GGTGGAAGAA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
Chromosome : 4
map
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
Position in Sequence : 1260389 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416.3
Amplified region : 1260005..1261237 in NT_006281
size : 1233
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycle

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : GCTAGAGTC CATTATCAGT C
BackwardPrimer : AGATTCCAT AATGTGGCAT G



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075355

12/17/2001

SNP Information



SNP Home

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SNP Information for IMS-JST075358

General Information

JSNP ID : IMS-JST075358
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	335985	4	68035987

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075358

12/17/2001

TCCTTTT

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GTCTAAATTT AACTTAGAAG AATATGGCAT TTAAGTGTGA AATACATTAC TTCCATTTAA
 Observed : G/A
 3' Assay : TAGTCTGTTT ATTGTGGCTT ATACACATAA TATATGTCAA AAATGTGTTA ATAATAACAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
 Chromosome : 4
 Map :
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 1263992 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416.4
 Amplified region : 1262944..1264128 in NT_006281
 size : 1185
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CTCCTACTATC ATCATGTCTG C
BackwardPrimer : TATTGAAAAC AGATCGTGGC



FOUO "SECRET"

SNP Information



SNP Home

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[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075359

General Information

JSNP ID : IMS-JST075359
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	333437	4	68033439

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	ST1B2	intron*1	Annotated	

TOGETHER

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTCAAAATGTC AGACTCTATT TAATTATAAA CCACCTTCCC AGATGTAAAA AATTATTCAA
Observed : A/T
3' Assay : TTTTAAAGC CTGAAAAATT TAAAGGTAA TACAATTAA AGACTGTTTG AATTCATTCA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 ([Graphical View of this Entry](#))
Chromosome : 4
map :
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
Position in Sequence : 1266540 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416_5
Amplified region : 1266274..1267183 in NT_006281
size : 910
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075359

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PCR "EFFECT"

Annealing : 60.0 degrees C for 0.50 minutes
 Polymerization : 72.0 degrees C for 2.00 minutes
 PCR Cycles : 35
 Post-Extension : 72.0 degrees C for 7.00 minutes
 ForwardPrimer : CACAGTTTTC CTGTGCTGAT G
 BackwardPrimer : TGGACCATGG TACTAGGGAG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075368

General Information

JSNP ID : IMS-JST075368
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	839825	2	105891956

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005224.2	genomic	SULT1C1	intron*1	Annotated	

TOPIC "SEQUENCE"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TACATGAGAC AGCCTGCTGC AGGCACATGG GGTCATCTC TGGCTGGCAG GAAGGTGAGG
Observed : G/C
3' Assay : AGTCCTCTCT TCTCTGGTCC TGGCTGACTC TGGCTCAGCA GGACTTCACT TGACCAATTCT
Comment : repeat sequence (repeat sequence exists in flanking sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_005224.2 (Graphical View of this Entry)
Chromosome : 2
map :
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
Position in Sequence : 1023481 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_005224.2.20010209_4
Amplified region : 1022386..1023623 in NT_005224
size : 1238
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

TOGETHER

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TGAGACAGTA GAAATCATGA C
BackwardPrimer : CTGCCTGATT CATCTGTTTA C



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SNP Information for IMS-JST075370

SNP Information



SNP Home

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[BLAST SNP](#)

[FTP Server](#)

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General Information

JSNP ID : IMS-JST075370
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	840639	2	105892770

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005224.2	genomic	SULT1C1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075370

12/17/2001

TOGETHER

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AAAAAGCTA AAGCTCTCCC CAAAGGAGGC CAGCGCGGT GGCTACGCC TCTAATCCCA
 Observed : G/C
 3' Assay : CACTTTGGGA GGCCGAGGCG SGTGATCAC AAGTCAGGA GATCGAGAGC ACGGTGAAAC
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_005224.2 (Graphical View of this Entry)
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 1022667 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_005224.2.20010209_5
 Amplified region : 1021644..1022832 in NT_005224
 size : 1189
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycle "E00T"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGAGTGCAGT AACCGTAGCT
BackwardPrimer : AGGTCAGGC AGAGTGGTTC



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075370

12/17/2001

T042347 "CE3500T"

SNP Information



SNP Home

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General Information

JSNP ID : IMS-JST075374
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	918099	2	105970230

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_005224.2	genomic	LOC65351	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075374

12/17/2001

NT_005224.2_20010209_7

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ACTTTCCAG GAGAGAGTGA AACAGTTAA GAGCAAAAGG GTAGACTTGT TTATTTATTC
Observed : A/C
3' Assay : TTCCCAATCT AGGCCCTTAT TGTAGATCTT GTAAAAAGCT GCATTGAGTG TGTGAGCTAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_005224.2 (Graphical View of this Entry)
Chromosome : 2
map :
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
Position in Sequence : 948390 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_005224.2_20010209_7
Amplified region : 947576..948773 in NT_005224
size : 1198
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

T024T "E3E00T

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CGACAGACAC CTGTGACATC
BackwardPrimer : CTTAAACCTC ATTAATGCCA TGA



SNP Information



SNP Home

[Search](#)

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[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075380

General Information

JSNP ID : IMS-JST075380
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_005224.5	924463	2	105976594

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AGCAGACAA CCTATGAGGT TATCAGTATA AAATCCCTT CTTTGTGTTT ACTTTGTTTT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075380

12/17/2001

TGAGTTCCTT

Observed : T/C
3' Assay : ACTTGGTACA AAAGTGTGT GCCACCATAC GAAGACTCCA GGCAGATGAT GTTCCCTAC
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_005224.2 (Graphical View of this Entry)
Chromosome : 2
map
Definition of the record : Homo sapiens chromosome 2 working draft sequence
e segment.
Position in Sequence : 1383482 ([View SNP position in this record](#))

Method

PCR Method
[Sequence Method](#)

PCR Profile

Screening region ID : NT_005224.2 20010209_9
Amplified region : 1383149..1384258 in NT_005224
size : 1110

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes

ForwardPrimer : CCTTGATCT CAACAGGTGC T

	1990	1991
1. Total population	100.0	100.0
2. Population aged 15 and over	75.0	75.0
3. Population aged 15 and over, female	37.5	37.5
4. Population aged 15 and over, male	37.5	37.5
5. Population aged 15 and over, female, 15-24	10.0	10.0
6. Population aged 15 and over, female, 25-34	10.0	10.0
7. Population aged 15 and over, female, 35-44	10.0	10.0
8. Population aged 15 and over, female, 45-54	10.0	10.0
9. Population aged 15 and over, female, 55-64	10.0	10.0
10. Population aged 15 and over, female, 65 and over	10.0	10.0
11. Population aged 15 and over, male, 15-24	10.0	10.0
12. Population aged 15 and over, male, 25-34	10.0	10.0
13. Population aged 15 and over, male, 35-44	10.0	10.0
14. Population aged 15 and over, male, 45-54	10.0	10.0
15. Population aged 15 and over, male, 55-64	10.0	10.0
16. Population aged 15 and over, male, 65 and over	10.0	10.0
17. Population aged 15 and over, female, 15-24, 25-34	20.0	20.0
18. Population aged 15 and over, female, 35-44, 45-54	20.0	20.0
19. Population aged 15 and over, female, 55-64, 65 and over	20.0	20.0
20. Population aged 15 and over, male, 15-24, 25-34	20.0	20.0
21. Population aged 15 and over, male, 35-44, 45-54	20.0	20.0
22. Population aged 15 and over, male, 55-64, 65 and over	20.0	20.0
23. Population aged 15 and over, female, 15-24, 25-34, 35-44	30.0	30.0
24. Population aged 15 and over, female, 45-54, 55-64, 65 and over	30.0	30.0
25. Population aged 15 and over, male, 15-24, 25-34, 35-44	30.0	30.0
26. Population aged 15 and over, male, 45-54, 55-64, 65 and over	30.0	30.0
27. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54	40.0	40.0
28. Population aged 15 and over, female, 55-64, 65 and over	20.0	20.0
29. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54	40.0	40.0
30. Population aged 15 and over, male, 55-64, 65 and over	20.0	20.0
31. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64	50.0	50.0
32. Population aged 15 and over, female, 65 and over	10.0	10.0
33. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64	50.0	50.0
34. Population aged 15 and over, male, 65 and over	10.0	10.0
35. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	60.0	60.0
36. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	60.0	60.0
37. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	70.0	70.0
38. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	70.0	70.0
39. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	80.0	80.0
40. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	80.0	80.0
41. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	90.0	90.0
42. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	90.0	90.0
43. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0
44. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0
45. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0
46. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0
47. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0
48. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0
49. Population aged 15 and over, female, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0
50. Population aged 15 and over, male, 15-24, 25-34, 35-44, 45-54, 55-64, 65 and over	100.0	100.0

[illegible]

TCCTTTCCTT

BackwardPrimer : ACAATGACAT ACAGTGCTA G



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075380

SNP Information



SNP Home

[Search](#)

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[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075427

General Information

JSNP ID : IMS-JST075427
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	1359216	19	64551367

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011190.3	genomic	SULT2A1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075427

12/17/2001

TOP SECRET

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GTGATCGGCC CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCATGAGC CACGGCGGCC
Observed : G/A
3' Assay : GCCAATTTAT CAGCTTTAAT TGCTCATCGC CCAGAACACT TCTCCCGTGG CCTCAGCAGG
Comment : repeat sequence (SNP is present in repeat sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_011190.3 (Graphical View of this Entry)
Chromosome : 19
map :
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
Position in Sequence : 1117678 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_011190.3.20010417.3
Amplified region : 1117026..1117896 in NT_011190
size : 871
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

Experiment 1

Annealing : 62.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CTGGGATTAC AGCGTGAAC
BackwardPrimer : TAGTTACCT GCTCACTGTC T



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075427

12/17/2001

SNP Information for IMS-JST075428

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword



General Information

JSNP ID : IMS-JST075428
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	1356250	19	64554333

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CCTGAAACCT TAAATATCAA ACCTCTGCAT CTCTGATCCC TTCCTTGTTA AAAGTTACCA

Sequence

Observed : G/C
 3' Assay : GGTGGCCAG GCRGGTGGT TCATGCCCTCT AATCCCAGCA CTATGGGAGG CCGAGACGGG
 Comment : repeat sequence (repeat sequence exists in flanking sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011190.3 (Graphical View of this Entry)
 Chromosome : 19
 map
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
 Position in Sequence : 1120644 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_011190.3.20010417_4
 Amplified region size : 1120220..1121152 in NT_011190 : 933

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGTGATAAC TATGTGACCA	G

TOGETHER

BackwardPrimer : TGACTCAACT CACTGCAAC



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075428

TOGETHER

SNP Information for IMS-JST075429

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST075429
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	1356237	19	64554346

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ATATCAAAAC TCATCATCTC TGATCCCTTC CTTGTTAAAA GTTACCASGG TTGGCCAGGC

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075429

12/17/2001

Sequence

Observed : A/G
 3' Assay : CCGTGGTTCA TGCCGTGTAAT CCGAGCACTA TGGGAGGCCG AGACGGCGG ATCACCAGGT
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011190.3 (Graphical View of this Entry)
 Chromosome : 19
 map
 Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
 Position in Sequence : 1120657 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011190.3.20010417_4
 Amplified region : 1120220..1121152 in NT_011190
 size : 933

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGTGAATAAC TATGTACCA	G

TSUBATA "CE3E00T"

SNP Information for IMS-JST075435

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075435
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	453137	19	65457446

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011190.3	genomic	SULT2B1	intron*1	Annotated	

NT_011190.3 "CEBCEOOT"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : AGGCAGCCCC AGGTTAGGAC CCAGACATGC GGATCCCAGG TTCCACGCTC CTCCTTTGGC
Observed : C/T
3' Assay : GAGTGCCTC CCTCCGCTGA CCCCTCTCCC CTGCTGCAG GACTTACAGG GTCCTCGTGA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_011190.3 ([Graphical View of this Entry](#))
Chromosome : 19
map
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
Position in Sequence : 82713 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_011190.3.20010417.8
Amplified region size : 82273..82895 in NT_011190 : 623
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : ACCTATTCCC TCCCACTAG
BackwardPrimer : GTCGTTGGGA GTTCTCTGGA



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075435

SNP Information for IMS-JST075436

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075436
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011190.5	451136	19	65459447

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011190.3	genomic	SULT2B1	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075436

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Top of the page

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GCGCCAATCA GCAATTGTT TGCAAGCCCT GAGCACAGAG CCTGCAGAAG GGGTCCCTT
Observed : C/T
3' Assay : CATGTCCAAG CAGTAATGGC TGCAGCATGG AGORTTGTGG GGGCATGAG ACAGGAGGCC
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_011190.3 (Graphical View of this Entry)
Chromosome : 19
map :
Definition of the record : Homo sapiens chromosome 19 working draft sequence segment.
Position in Sequence : 80712 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_011190.3_20010417_9
Amplified region : 79864..80803 in NT_011190
size : 940
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075436

12/17/2001

PCR "E63E00T"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : AGGCTTGGAG GGTTCCTGAG
BackwardPrimer : CTGCAGCACC TTGGCCTCTG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075436

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



SNP Information for IMS-JST075486

General Information

JSNP ID : IMS-JST075486
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	10166541	22	27418329

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GAGGAGACTG AGGCTTAGGG AGGGTGAGGT TCATAGCTTC ATGCCTAAGT TTACAGTAGC

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075486

12/17/2001

Sequence

Observed : T/C
 3' Assay : AGGCAGGAAA GGCACAACCA GCCTTGGACC COTCAGTGG CTGGACGGG AGGCACGGAC
 Comment : repeat sequence (SNP is present in repeat sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_011520.5 (Graphical View of this Entry)
 Chromosome : 22
 map
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 10168640 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_011520.5.20010417_12
 Amplified region : 10168482..10169592 in NT_011520
 size : 1111

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TAGGTCTCCT ACACAGGATC	

Footnote

BackwardPrimer : GGACAGGAAG CTCTATCCTG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075486

12/17/2001

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SNP Information for IMS-JST075493

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075493
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011520.7	10160723	22	27412511

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_011520.5	genomic	CST	CDS*1	Annotated	

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SupInfo.cgi?SNP_ID=IMS-JST075493

Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.4	0	1
Exercise frequency	2.5	1.5	0	5
Stress level	3.5	1.5	1	5
Sleep quality	4.0	1.0	2	5
Work satisfaction	3.0	1.0	1	5
Life satisfaction	4.5	1.0	2	5

Allele Sequence

Variation Type	:	SNP
Flanking Sequence	:	Information
5' Assay	:	GGAGGCGCA
Observed	:	C/T
3' Assay	:	GGTCTGCTGCT
Comment	:	GGGAGTGCCA
Sample size	:	96
		CTCCACCTGC
		ACTCGAGCCA
		GAGGCACTGA
		TCCGGGCGCAA
		GGCGCGGCGC
		AACATCGTGT
		TCTTGAAGAC
		GCACAAGACG

Screened Sequence

Accession No.	:	NT_011520.5	(Graphical View of this Entry)
Chromosome	:	22	
map	:		
Definition of the record	:	Homo sapiens chromosome 22 working draft sequence segment.	
Position in Sequence	:	10162832	(View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID	:	NT_011520.5_20010417_16	
Amplified region	:	10162183..10163173 in NT_011520	
size	:	991	
Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075493

12/17/2001

PCR METHOD

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TGGTACATGC AACACAGTGG
BackwardPrimer : GTTGAGCTTG AAGTAGAGCA C



12/17/2001

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FOR "SECRET"

SNP Information for IMS-JST075563

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075563
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	402804	4	68102806

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTTTATTAT TAATATCAAT ACTTAGATTT TAGATATATA AAATATAGAA TGAAAAATTAT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075563

12/17/2001

TOGETHER

Observed : G/A
 3' Assay : TATTACAAAG CTCTTAAAAA TAAATATATAC AAAGACCAAA GTCTTGATTG ATACTTAGT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
 Chromosome : 4
 map
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 1197173 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

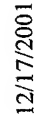
Screening region ID : NT_006281.3.20010416.8
 Amplified region : 1196916..1197777 in NT_006281
 size : 862

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GGTCTGATTG AGGTCCTTG	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST075563

12/17/2001

BackwardPrimer : ACCTCCTTCT ACCCTGCTTG



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SNP Information for IMS-JST075565

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

General Information

JSNP ID : IMS-JST075565
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403390	4	68103392

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GAACATGTA CAAAAGTCAC TTTTGCCTCA TACAGGTAAA TCTAGAAAG TAGGGACTAT

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075565

PCR "E3E00"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CGTCTCTGCC TCCTTTAATG
BackwardPrimer : GACAACCAGA TGATGAGGTG



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075539

THE "SECRET" DATABASE

SNP Information for IMS-JST075566

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075566
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403406	4	68103408

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TCACCTTTGC CTCATACAGG TAAATCTAAG AAAGTAGGGA CTATGAGAAC CCCATATGTAT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075566

12/17/2001

NT_006281.3

Observed : C/T
3' Assay : TATATCCACC ATAGTATTCT AGCACTGACT ACAGGGGCTA GGAAGGGT AGGCATTAC
Comment : repeat sequence (SNP is present in repeat sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
Chromosome : 4
map
Definition of the record : Homo sapiens chromosome 4 working draft sequence
Position in Sequence : 1196571 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416_9
Amplified region : 1196173..1197306 in NT_006281
size : 1134

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GATCTGCCTT GTATTGTAA	G

BackwardPrimer : GAGGCAAGT AGTGGCATG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075566

12/17/2001

FOOTNOTES

SNP Information for IMS-JST075567

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST075567
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403507	4	68103509

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GGAAAAGGGT AGGCATTTCAC ATAGGGAGTA TTGCTGGAT AAAAGGCAGG TTGGAAGATG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075567

12/17/2001

TOP SCREEN

Observed : C/A
 3' Assay : AGGAGGGGAG TATGAGAAA GAAAGGAAGA AAGAGAGGAA GGAGAGCGG AAGGAAAAAC
 Comment : repeat sequence (repeat sequence exists in flanking sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
 Chromosome : 4
 map :
 Definition of the record : Homo sapiens chromosome 4 working draft sequence
 e segment.
 Position in Sequence : 1196470 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3 20010416_9
 Amplified region : 1196173..1197306 in NT_006281
 size : 1134

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GATCTGCCTT GGTATTGAA G	

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075567

General Information

JSNP ID : IMS-JST075567
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	403507	4	68103509

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GGAAGAAGGGT AGGCATTAC ATAGGAGTA TTTCGTGGAT AAAAGGCAGG TTGGAAGATG

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075567

12/17/2001

TTGGTTTGGGGT

Observed : C/A
 3' Assay : AGGAGGGGAG TATGCAGAAA GARAGGAAGA AAGAGAGGAA GGAGAGCGGG AAGGAAAAAC
 Comment : repeat sequence (repeat sequence exists in flanking sequence)
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
 Chromosome : 4
 map :
 Definition of the record : Homo sapiens chromosome 4 working draft sequence
 e segment.
 Position in Sequence : 1196470 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416.9
 Amplified region : 1196173..1197306 in NT_006281
 size : 1134

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GATCTGCCTT GGTATTGAA G	

Sequence = CCGGGGT

BackwardPrimer : GAGGCAAAGT AGTGGCATG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075567

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075568

General Information

JSNP ID : IMS-JST075568
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	404450	4	68104452

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AATAGATTGT CATGGGATCA GGAGATGAAT TAGGAAATGA TAACCATCTT GCTTAACCTT

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12/17/2001

Observed : A/G
3' Assay : TCATTTTATG CCAAGTCATT CAATGGGAGT ATCCACTACC TTATTCATCG AATGGGGAAA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
Chromosome : 4
map
Definition of the record : Homo sapiens chromosome 4 working draft sequence
e segment.
Position in Sequence : 1195527 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416.10
Amplified region : 1194357..1195580 in NT_006281
size : 1224

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extention	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TGTCATGGGA TCAGGAGATG	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075568

12/17/2001

TTGGTTT " CCGGGGGT

BackwardPrimer : AATGGTGGTC ATACGCTGTA



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12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075569

General Information

JSNP ID : IMS-JST075569
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	404663	4	68104665

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TCCTTTAAAT ACATTCACCA AGCATTTGGT TTATTTAAAA AAATGATACA TATTCAGGAA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075569

12/17/2001

TACAAATCTCTGACTTAGA TACCYGGCAA TAAATATCAA ATGTAATGAT CTTATTGTT

Observed : A/G
3' Assay : TCAAAATCTCTGACTTAGA TACCYGGCAA TAAATATCAA ATGTAATGAT CTTATTGTT
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
Chromosome : 4
map
Definition of the record : Homo sapiens chromosome 4 working draft sequence
e segment.
Position in Sequence : 1195314 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416.10
Amplified region : 1194357..1195580 in NT_006281
size : 1224

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TGTCATGGGA TCAGGAGATG	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075569

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST075577

General Information

JSNP ID : IMS-JST075577
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	410462	4	68110464

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

Top of the page

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TACAAAAGTC TGAAGTAACA TAGAAGTAAT GATCAATGAC TACATGAACT TAGAGAATCA
 Observed : A/G
 3' Assay : GTAGATCACA CACACCAACA ATAAATTAC ACAGATGAT AAAAGAATTT GAATGGAGAG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
 Chromosome : 4
 map :
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 1189515 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416_13
 Amplified region : 1189368..1190522 in NT_006281
 size : 1155
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
 Polymerization : 72.0 degrees C for 2.00 minutes
 PCR Cycles : 35
 Post-Extension : 72.0 degrees C for 7.00 minutes
 ForwardPrimer : AGCTGACGGT TTACACTGTC
 BackwardPrimer : TATACCTCTC CTATCTGATG C



Top of Page

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075579

General Information

JSNP ID : IMS-JST075579
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	414009	4	68114011

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

TTCTGATCAT GTAGTAACAA

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : AAGAAAGGGT GCAGNATAGT CTAGTATCTA AAGAAGGCCA TTCTGATCAT GTAGTAACAA
 Observed : T/C
 3' Assay : TATAAAGAAA ATAATAATGT GTTTTCATAT CCACAGATGA TAATATTGAC TCAAGACAAA
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 ([Graphical View of this Entry](#))
 Chromosome : 4
 map
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 1185968 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006281.3 20010416_14
 Amplified region : 1185499..1186704 in NT_006281
 size : 1206
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Cycling Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TCTAATGGTG GCTGGTCATC
BackwardPrimer : CCCTTAGTGT CATCTCACT C



FOR "CE3E00T"

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST075580

General Information

JSNP ID : IMS-JST075580
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	414325	4	68114327

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

TTTGGGTT "GGGGGGT

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CTAATGGAGT CAAAGAACAG AGGAGGCATA CAATGACTTC AGGCAAAGCA GAACCTTTTG
 Observed : A/C
 3' Assay : CTCACACAAC ATTATATTAT TTTGTCAGCT TTATATTTTA TGAACAATT TTTACTATGAG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 ([Graphical View of this Entry](#))
 Chromosome : 4
 map :
 Definition of the record : Homo sapiens chromosome 4 working draft sequence
 e segment.
 Position in Sequence : 1185652 ([View SNP position in this record](#))

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416.14
 Amplified region : 1185499..1186704 in NT_006281
 size : 1206
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : TCTAATGGTG GCTGGTCATC
BackwardPrimer : CCTTAGTGT CATTCTCACT C



12/17/2001 12:33:00

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

search

SNP Information for IMS-JST075584

General Information

JSNP ID : IMS-JST075584
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006281.5	419468	4	68119470

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006281.3	genomic	STE	intron*1	Annotated	

Top of the page

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TTGATTATA TGTTCCTTT TTCAAAATTC TACATATAAA TGTACAGAG GACTTAAAC
 Observed : A/G
 3' Assay : GTTGCTTGC TTGCAACGG TGAAGTCTG CTGTACCCTC AGAACCTATC TGATTTTTT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006281.3 (Graphical View of this Entry)
 Chromosome : 4
 map :
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 1180509 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006281.3.20010416.15
 Amplified region : 1180366..1181496 in NT_006281
 size : 1131
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

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12/17/2001

Test Results

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : CATCAGAGGA GCTTGTTGGAC
BackwardPrimer : GTTCACTTGC CCTCTTGCTC



12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IS7075584

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST105158

General Information

JSNP ID : IMS-JST105158
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007402.5	1061191	6	56512411

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TCCTTTCTG GACAGTCATT TTATTCTGA TAAAGCGTT CTTCTTATG CATTGCAAA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105158

12/17/2001

TCCTGCTGT

BackwardPrimer : AGGTGGAGAT TCCTGCTGT



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551

12/17/2001

TTGGTTTGGGGGTT

BackwardPrimer : CCTGGGAGAG ATTAGCACTA



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12/17/2001

FOR THE "GENE" PROJECT

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

SNP Information for IMS-JST105159

General Information

JSNP ID : IMS-JST105159
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007402.5	857593	6	56716009

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GTGGGTATT TTTTAAAC CCTTCTGCG GAGTCTGAAT GCATTGGTGG AAGTGGGCT

TOGETHER

Observed : C/T
3' Assay : GGATCGTCCC CGGGCCTGGC TGGGCTGCCG CTACGCCCTC GCATGGGCTG AGCGGGGAAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_007343.3 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Homo sapiens chromosome 6 working draft sequence
Position in Sequence : 2411915 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_007343.3.20010416.7
Amplified region : 2411339..2412239 in NT_007343
size : 901

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TCGTACTAGA GCTTCAGCAG	

T04331T "EE3E00T

BackwardPrimer : GGAAATCGC ACAGCCACTG



[http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=\[MS-IST105159](http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=[MS-IST105159)

12/17/2001

TOP "6633E00F"

SNP Information for IMS-JST105163

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105163
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_007402.5	869160	6	56704442

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_007343.3	genomic	GSTA4	intron*1	Annotated	

TCAGAT " CCGGCGT

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ATATTTGACC TGGAAATTGTG TTGGGAGTCC CTCTGACACA CACACTTGTG CACATGCAGA
Observed : C/T
3' Assay : ACCCATGGC ATCCAAGAGT TGACTGTGAA GGGGATCTCC CCTTTGCTAC YACTGCTTCT
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_007343.3 (Graphical View of this Entry)
Chromosome : 6
map
Definition of the record : Homo sapiens chromosome 6 working draft sequence segment.
Position in Sequence : 2423482 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_007343.3.20010416.11
Amplified region : 2423025..2424109 in NT_007343
size : 1085
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR "SEQUENCE"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GACCATCTTT ATGGAAGTAG AT
BackwardPrimer : GCAGTATCTG AGAAGAGGTG



SNP Information for IMS-JST105069

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105069
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004966.5	3635060	1	114067278

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_004966.3	genomic	GSTM4	intron*1	Annotated	

NT_004966.3 "CE3600"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GTGACAGTAT TCTTATTCA GTCCTGCCAT GAGCAGGCAC AGTGAGTGCC CGGTCTCCTC
Observed : T/C
3' Assay : CTGCTCTTGC TTATGGGAG GGGATGCTGG GGAGCCTGTT GGCCCAACTG AGCTTCGGCG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_004966.3 ([Graphical View of this Entry](#))
Chromosome : 1
map
Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.
Position in Sequence : 493791 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_004966.3.20010416.3
Amplified region : 492835..493989 in NT_004966
size : 1155
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

PCR Conditions

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : GTGCAACGTG TCTCTGACTG
BackwardPrimer : AGGAGCTCA GGGAAAGTAG



Top of the page

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword



SNP Information for IMS-JST075522

General Information

JSNP ID : IMS-JST075522
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2733857	2	98509980

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : GGGAAACCCGC GGGTTTGTGC CTGGCGAGCC ACATCCCGGT GTGTTTGGC GACTTGAAGA

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12/17/2001

NT_022171.2

Observed : C/T
 3' Assay : CTCCTAGTT GCGGGAGTA GCGGGAAGAG CCTTCTCTGC GTTAATTATG CAATAAGAAAG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 (Graphical View of this Entry)
 Chromosome : 2
 map :
 Definition of the record : Homo sapiens chromosome 2 working draft sequence
 Position in Sequence : 526155 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_022171.2.20010209_1
 Amplified region : 525548..526488 in NT_022171
 size : 941

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TTTTCGTGAT GGAGGCCAG C	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075522

12/17/2001

CTCTGACAG CGAAGATCAG

BackwardPrimer : CTCTGACAG CGAAGATCAG



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12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword



SNP Information for IMS-JST075524

General Information

JSNP ID : IMS-JST075524
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2732905	2	98509028

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ATGAAAATTG GAGTGTGTTGC AAAACTGAAC AAAGAAAGGA AAGAATTTGT AACATCACACA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075524

12/17/2001

TTGAGT " CCGGCT

Observed : G/A
3' Assay : GCAACTTGCA GTTATATCG GATCATTTTT CAGTGTTTGA GGAGTTCATA CAATAAAAAAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 (Graphical View of this Entry)
Chromosome : 2
map
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
Position in Sequence : 527107 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_022171.2 20010209_2
Amplified region : 526278..527279 in NT_022171
size : 1002

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extention	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CTTCTTTCAT CCTTGGCTGA	G

Forward Primer : CAGGAGGTT ATCCAGAAAGT G

BackwardPrimer : CATCCAGGTT ATCCAGAAAGT G



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12/17/2001

SNP Information



SNP Home

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BLAST SNP

FTP Server

Search Example

Keyword

1000 JOURNAL OF DOCUMENTATION

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SNP Information for IMS-JST075527

General Information

JSNP ID	:	IMS-JST075527
dbSNP ID(rs#)	:	
dbSNP ID(ss#)	:	
HGBASE ID	:	
Organism	:	Homo sapiens
Molecular type	:	Genomic
Laboratory	:	Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation	:	<u>J Hum Genet. 2001;46(4):225-40</u>
Release Date	:	2001/06/11
Last Update	:	2001/06/11

NEW
Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2731721	2	98507844

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TCTTTGAACT TTTAATAATG CTTTTTTTTT TTTTAATTTTC CTATCCAGTG ACAAGAGGAA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075527

12/17/2001

NT_022171.2

Observed : C/A
 3' Assay : CAAGAACCTC AGTTCAGGGG AAACACAGCA AGGAATGTC AGCCCCAGGC TGCAGAGGT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 (Graphical View of this Entry)
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 528291 ([View SNP position in this record](#))

Method

[PCR Method](#)
[Sequence Method](#)

PCR Profile

Screening region ID : NT_022171.2.20010209_3
 Amplified region : 527752..528439 in NT_022171
 size : 688

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CCCAGTCAGC TTGGGCTTTA	T

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075527

12/17/2001

TTTACAATCT GCACAGGCAA G

BackwardPrimer : TTTACAATCT GCACAGGCAA G



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075527

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075539

General Information

JSNP ID : IMS-JST075539
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2662111	2	98438234

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_022171.2	genomic	HNK-1ST	intron*1	Annotated	

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : GGGGAGGACA GCAAGGAGGA GTCACAAGAG GGCTGGTTTG ACCTGAAGGG ACTGGTGGCC
 Observed : G/T
 3' Assay : TCCAGACAGG CCTGTTTTTG TTGTTTCCTG TTAGTGTTCT GCCTTACAAG TTAGTGGGGC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 ([Graphical View of this Entry](#))
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 541579 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_022171.2.20010209.9
 Amplified region : 541167..542399 in NT_022171
 size : 1233
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

PCR "E3E00"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : CGTCTCTGCC TCCTTTAATG
BackwardPrimer : GACAACCAGA TGATGAGGTG



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http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075539

TOP222T" E6633E00T

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

SNP Information for IMS-JST075548

General Information

JSNP ID : IMS-JST075548
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2657464	2	98433587

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : ACCAGGTGAA GATCTGAGCC CAGAAATGAC CCTTCCTCCA CCACACCCCT CCTTTGAGGA

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075548

12/17/2001

Sequence

Observed : C/T
 3' Assay : GCCCGGGGTC TCCACAGGC CTGTGAGTTG CCTCGGCATA TGACGCAGAA CCCCCACTGT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 (Graphical View of this Entry)
 Chromosome : 2
 map
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 546226 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_022171.2 20010209_13
 Amplified region : 545838..547022 in NT_022171
 size : 1185

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGACGTATG TAGAGCTCTG	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075548

12/17/2001

[illegible]

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SNP Information for IMS-JST075551

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST075551
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2657102	2	98433225

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TGCAGGAACA GCACCCAGGA CTCTGAGGAG GGACAGAGAA GCAAGGGGGC TGCTGAAATC

12/17/2001

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551

TOP LEFT: 44336007

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

Keyword

Search

SNP Information for IMS-JST075551

General Information

JSNP ID : IMS-JST075551
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HGBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(4):225-40
 Release Date : 2001/06/11
 Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2657102	2	98433225

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TGCAGGAACA GCACCCAGGA CTCTGAGGAG GGACAGAGAA GCAAGGGGGC TGCTGAAATC

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551

12/17/2001

TTGAGTTTGGGGGGT

Observed : G/C
3' Assay : CAGAGACTTT TGCAGCATCA GATCTGAGGA GTAAAACGGC ACCTCTGGCC TTCATCTTGG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 (Graphical View of this Entry)
Chromosome : 2
map
Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
Position in Sequence : 546588 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_022171.2.20010209.13
Amplified region size : 545838..547022 in NT_022171 : 1185
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : GTGACGTATG TAGAGCTCTG

TCCTGCTGT

BackwardPrimer : AGGTGGAGAT TCCTGCTGT



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075551

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075553

General Information

JSTP ID : IMS-JST075553
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information **NEW**

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_022171.5	2656813	2	98432936

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTCATTTCAGC ACAAGACATA CGATTTTGA AGGTGAGGG AGGGAGGCT TTTTCTACCT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075553

12/17/2001

TOGETHER WE CAN SAVE THE WORLD

Observed : G/A
 3' Assay : AGAAGGGGAG TGTCCTTTGAG GGCCTTAAAA GGACCATGGC CCAGGAATGG GGGCGCTGGT
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_022171.2 (Graphical View of this Entry)
 Chromosome : 2
 map :
 Definition of the record : Homo sapiens chromosome 2 working draft sequence segment.
 Position in Sequence : 546877 ([View SNP position in this record](#))

Method

[PCR Method](#)
[Sequence Method](#)

PCR Profile

Screening region ID : NT_022171.2 20010209_13
 Amplified region : 545838..547022 in NT_022171
 size : 1185

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	GTGACGTATG TAGAGCTCTG	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075553

12/17/2001

TTTGGT " CCGGGGT

BackwardPrimer : AGGTGGAGAT TCACTGCTGT



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075553

12/17/2001

SNP Information for IMS-JST105117

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105117
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_008541.5	4035179	9	83945560
NT_008541.5	5158989	9	82821750

Gene Information

Allele Sequence

Variation Type : SNP

Flanking Sequence Information

5' Assay : CTGCGCCTCC ATGGCTCTGC AGATCCTCTG GGAAGCGGCC CGCCACCTGT GACCAGCAGC
Observed : T/G
3' Assay : GATGCCCTCT TGGCCACCAG ACCATGGGCC AAGAGCCGCC GTGGCTATAC CTGGGGACTT
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_008541.3 (Graphical View of this Entry)
Chromosome : 9
map
Definition of the record : Homo sapiens chromosome 9 working draft sequence segment.
Position in Sequence : 589170 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_008541.3 20010416_2
Amplified region : 588076..589240 in NT_008541
size : 1165
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes
Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

Footnote

ForwardPrimer : AACCAGCAGA AGTAGGTGAG
BackwardPrimer : AAGGAACATC AGTCCCCAG



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http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105117

TOGETHER

SNP Information for IMS-JST105119

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105119
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	495606	4	138937022

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

NT_006124.3

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TTGCAGGTAG CTCCTGGTCC TCAGAGCACA GTCCGCTCAG GGTCACCCAT GCCGCCGTGCT
 Observed : A/C
 3' Assay : CCCTCCTTCC CAGGGCAAG CAGAGACYGA GATCATTCCA GAGATTAGTT CTCCCAACTG
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : NT_006124.3 ([Graphical View of this Entry](#))
 Chromosome : 4
 map
 Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
 Position in Sequence : 495592 (View SNP position in this record)

Method

PCR Method
 Sequence Method

PCR Profile

Screening region ID : NT_006124.3.20010416.1
 Amplified region : 495156..496414 in NT_006124
 size : 1259
 Pre-Denature : 94.0 degrees C for 2.00 minutes
 Denaturation : 94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105119

12/17/2001

PCR "EFFECT"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCACAGTCTC TAGGTGACAG
BackwardPrimer : CAAATGTGAC TCCCATGGAG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105119

12/17/2001

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

search

SNP Information for IMS-JST105120

General Information

JSNP ID : IMS-JST105120
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	495578	4	138937050

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

Allele Sequence

Variation Type	:	SNP
Flanking Sequence	:	Information
5' Assay	:	CAGTCGGCTC
Observed	:	T/C
3' Assay	:	GAGAACATTC
Comment	:	CAGAGATTAG TTCTCCCAAC TGGAACGCTG TGGGGCCTCA GAGCTCAGCG
Sample size	:	96

Screened Sequence

Accession No.	:	NT_006124.3	(Graphical View of this Entry)
Chromosome	:	4	
map	:		
Definition of the record	:	Homo sapiens chromosome 4 working draft sequence segment.	
Position in Sequence	:	499564	(view SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID	:	NT_006124.3_20010416_1
Amplified region	:	495156..496414 in NT_006124
size	:	1259
Pre-Denature	:	94.0 degrees C for 2.00 minutes
Denaturation	:	94.0 degrees C for 0.50 minutes

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105120

12/17/2001

PCR REACTION

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes

ForwardPrimer : TCAGAGTCTC TAGTGACAG
BackwardPrimer : CAAATGTGAC TCCCATGGAG



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105120

12/17/2001

TOGETHER "CE3E00T"

SNP Information for IMS-JST105126

SNP Information



SNP Home

Search

Search by HOWDY

BLAST SNP

FTP Server

Search Example

General Information

JSNP ID : IMS-JST105126
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword

search

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	468656	4	138963972

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

NT_006124.3 "CEB3E00T"

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TGGCGCGGT GGCTCAGCC TGTAATCCA GCACTTGGG AGGCCGAGGT GGGCGGATCA
Observed : T/C
3' Assay : GAGTCAGGA GATCGAGACC ACGATGAAC CCGTCTCTA CTAAATATC AAAAAATTAG
Comment : repeat sequence (SNP is present in repeat sequence)
Sample size : 96

Screened Sequence

Accession No. : NT_006124.3 (Graphical View of this Entry)
Chromosome : 4
map
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
Position in Sequence : 468642 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006124.3 20010416_6
Amplified region : 467851..468999 in NT_006124
size : 1149
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

12/17/2001

TCTGAT "CCCCCT"

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : GCAGTGCAGT TTGGACTTAG
BackwardPrimer : GAAAGACATG GCTGAGGTAG



SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST105129

General Information

JSNP ID : IMS-JST105129
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_006124.5	466132	4	138966496

Gene Information

Relation to gene sources

Database ID	Type	Gene	In Gene	Evidence	Locus Link ID
NT_006124.3	genomic	MGST2	intron*1	Annotated	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105129

12/17/2001

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : CTACCAATCC TGGAGACTAA ACAAATAAA CAGTGTGTGC ATCAGAGTGC TATGTTGCAG
Observed : A/G
3' Assay : TATATGAACT TTGGCTTCAT TCTAATTTAA TTCAATAATG AAAAAAATAT TGAGACAAAC
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_006124.3 (Graphical View of this Entry)
Chromosome : 4
map :
Definition of the record : Homo sapiens chromosome 4 working draft sequence segment.
Position in Sequence : 466118 (View SNP position in this record)

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_006124.3.20010416.7
Amplified region : 466019..467240 in NT_006124
size : 1222
Pre-Denature : 94.0 degrees C for 2.00 minutes
Denaturation : 94.0 degrees C for 0.50 minutes

--- SNP INFORMATION ---

PCR REACTION

Annealing : 60.0 degrees C for 0.50 minutes
Polymerization : 72.0 degrees C for 2.00 minutes
PCR Cycles : 35
Post-Extension : 72.0 degrees C for 7.00 minutes
ForwardPrimer : ACGTCTTCTA TGAATAGAGG C
BackwardPrimer : AAGTCATGT CGTTCATTT C



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-IST105129

12/17/2001

SNP Information for IMS-JST105136

SNP Information



SNP Home

[Search](#)

[Search by HOWDY](#)

[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

General Information

JSNP ID : IMS-JST105136
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HCBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(7):385-407
Release Date : 2001/08/09
Last Update : 2001/08/09

Keyword



Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004648.5	2300671	1	165016888

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : AAATTAGCA GTTAGCAGCA AGTAGATTAT CGCTATGTAA AATAAAATTC CTGAGTTTCT

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105136

12/17/2001

Sequence

Observed : G/C
3' Assay : TCACTCGCTC TTACAGTACC TACCTGCCTA CCTGCCTCTG AGGAGAAACG CTGTAATTAG
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_004648.3 (Graphical View of this Entry)
Chromosome : 1
map
Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.
Position in Sequence : 422012 ([View SNP position in this record](#))

Method

PCR Method
[Sequence Method](#)

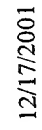
PCR Profile

Screening region ID : NT_004648.3 20010416_3
Amplified region : 421033..422147 in NT_004648
size : 1115

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CGAAGAATAT ACTGCTACGG	T

12/17/2001

BackwardPrimer : AGTTGACCA CACCTGACAT C



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105136

SNP Information for IMS-JST105137

SNP Information



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[BLAST SNP](#)

[FTP Server](#)

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General Information

JSNP ID : IMS-JST105137
 dbSNP ID(rs#) :
 dbSNP ID(ss#) :
 HCBASE ID :
 Organism : Homo sapiens
 Molecular type : Genomic
 Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
 Citation : J Hum Genet. 2001;46(7):385-407
 Release Date : 2001/08/09
 Last Update : 2001/08/09

Keyword

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_004648.5	2300743	1	165016960

Gene Information

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : TACAGTACCT ACCTGCCTAC CTGCCTCTGA GGAGAAACGC TGTATTAGG CAACAGGAAA

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12/17/2001

Observed : A/G
 3' Assay : TTGTAATATC TTTCAAATGC ATTGCAAT GCCTTTAAGG ATTTATCCT TTAGAATCAT
 Comment :
 Sample size : 96

TTTCAAATGC ATTGCAAT GCCTTTAAGG ATTTATCCT TTAGAATCAT

Screened Sequence

Accession No. : NT_004648.3 (Graphical View of this Entry)
 Chromosome : 1
 map
 Definition of the record : Homo sapiens chromosome 1 working draft sequence segment.
 Position in Sequence : 421940 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_004648.3 20010416_3
 Amplified region : 421033..422147 in NT_004648
 size : 1115

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	CGAAGAATAT ACTGCTACGG	T

[illegible]

BackwardPrimer : AGTTGACCA CACCTGACAT C



http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105137

12/17/2001

SNP Information



SNP Home

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[BLAST SNP](#)

[FTP Server](#)

[Search Example](#)

Keyword

SNP Information for IMS-JST075388

General Information

JSNP ID : IMS-JST075388
dbSNP ID(rs#) :
dbSNP ID(ss#) :
HGBASE ID :
Organism : Homo sapiens
Molecular type : Genomic
Laboratory : Laboratory for Genotyping, The SNP Research Center, RIKEN
Citation : J Hum Genet. 2001;46(4):225-40
Release Date : 2001/06/11
Last Update : 2001/06/11

Mapping Information NEW

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_011521.1	334554	22	40632693

Gene Information

Locus Link ID : 25830
Gene Name : sulfortranferase family 4A, member 1
Gene symbol : SULT4A1
Alias symbol : SULTX3, BR-STL-1, DJ388M5.3
Product : sulfortranferase family 4A, member 1

Relation to gene sources

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST075388

12/17/2001

Sequence

NT_011521.1	genomic	SULT4A1	intron*1	Annotated
Hs.189810	mRNA	SULT4A1	intron*3	Homology
				25830

view predicted exons with Unigene : [Hs.189810](#)

Allele Sequence

Variation Type : SNP
 Flanking Sequence Information
 5' Assay : CAGTGTGACT GTGTATGGT TAGCAGGGAG CGGCTCCTA GCCTGGGCTT CTGGAGGGAG
 Observed : C/T
 3' Assay : GAGAGGAGAG TGGAGGGCCC ATTGAGAGGT GGAAGCCTCC CTAAGCATG CTTTGGAGAC
 Comment :
 Sample size : 96

Screened Sequence

Accession No. : [NT_011521.1](#) ([Graphical View of this Entry](#))
 Chromosome : 22
 map :
 Definition of the record : Homo sapiens chromosome 22 working draft sequence segment.
 Position in Sequence : 334554 (view SNP position in this record)

Method

PCR Method
 Sequence Method

NT_011521.1 20010416_4

PCR Profile

Screening region ID : NT_011521.1 20010416_4
Amplified region : 334027..335031 in NT_011521
size : 1005

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	TAGGTCTGGA GAAGAGCCTG T	
BackwardPrimer	:	GCATCAGCAG CAGCGACGAT G	



SNP Information for IMS-JST105400



Search

BLAST SNP

FTP Server

Search Example

Keyword

search

NEW Mapping Information

Contig ID	Contig Position	Chromosome	Chromosome Position
NT_019583.5	2782880	14	20567815

Gene Information

Allele Sequence

Variation Type : SNP
Flanking Sequence Information
5' Assay : TTTCAATGGAT TGCTTTCCCTG ACTTGAGGTT CACATGTTTG AAATTTACCC TAACCAACCT

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TOGETHER

Observed : G/C
3' Assay : ACTCTCTGCC ACTTTCTGTGTC TCTGTCCTTG TCTGTCCTGGA GGAAGGAGGA GGGTAGATTA
Comment :
Sample size : 96

Screened Sequence

Accession No. : NT_019583.3 (Graphical View of this Entry)
Chromosome : 14
map
Definition of the record : Homo sapiens chromosome 14 working draft sequence segment.
Position in Sequence : 3336512 ([View SNP position in this record](#))

Method

PCR Method
Sequence Method

PCR Profile

Screening region ID : NT_019583.3 20010417_3
Amplified region : 3335968..3337267 in NT_019583
size : 1300

Pre-Denature	:	94.0 degrees C for	2.00 minutes
Denaturation	:	94.0 degrees C for	0.50 minutes
Annealing	:	60.0 degrees C for	0.50 minutes
Polymerization	:	72.0 degrees C for	2.00 minutes
PCR Cycles	:	35	
Post-Extension	:	72.0 degrees C for	7.00 minutes
ForwardPrimer	:	AGCTGTAACA CTCACTGCCGA	

http://snp.ims.u-tokyo.ac.jp/cgi-bin/SnpInfo.cgi?SNP_ID=IMS-JST105400

12/17/2001

TGAGGTTTGGGGGGT

BackwardPrimer : GTGAGTTCAT GGTCTCAGGA

